

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | : | |
Db 1 FPDKKHKL 8

RESULT 37
ABJ43122

ID ABJ43122 standard; peptide; 9 AA.
XX
AC ABJ43122;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #942.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 167; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | : | |
Db 1 FPDKKHKL 8

RESULT 38
ABJ46322

ID ABJ46322 standard; peptide; 9 AA.
XX

AC ABJ46322;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #4142.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 198; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
| | | : | |
Db 2 FPDKKHKL 9

RESULT 39
ABJ47111

ID ABJ47111 standard; peptide; 9 AA.
XX
AC ABJ47111;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #4931.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.

XX WO200283860-A2.
XX 24-OCT-2002.
XX 09-APR-2002; 2002WO-US011644.
XX 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX Claim 13; Page 206; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX a molecule that is modulated by the 151P3D4 protein, where the status of
XX a cell that expresses the 151P3D4 protein is modulated. The novel
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX a humoral or cellular immune response. The 151P3D4 genes and proteins
XX are also useful for diagnosing, prognosing, preventing or treating
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX human leukocyte antigen peptide relating to the 151P3D4 composition of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FPDENFKL 9
XX |||: ||
XX Db 1 FPDKKHKL 8
XX
XX
XX RESULT 40
XX ABJ48392
XX ID ABJ48392 standard; peptide; 9 AA.
XX AC ABJ48392;
XX
XX DT 16-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related HLA peptide #6212.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
XX OS Homo sapiens.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX PA

XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX Claim 13; Page 218; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX a molecule that is modulated by the 151P3D4 protein, where the status of
XX a cell that expresses the 151P3D4 protein is modulated. The novel
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX a humoral or cellular immune response. The 151P3D4 genes and proteins
XX are also useful for diagnosing, prognosing, preventing or treating
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX human leukocyte antigen peptide relating to the 151P3D4 composition of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FPDENFKL 9
XX |||: ||
XX Db 2 FPDKKHKL 9
XX
XX
XX RESULT 41
XX ABJ39852
XX ID ABJ39852 standard; peptide; 9 AA.
XX AC ABJ39852;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related peptide #479.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX bronchial; breast; carcinoma.
XX
XX OS Unidentified.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX PA
XX PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX

PS Claim 13; Page 131; 426pp; English.

XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or

CC a molecule that is modulated by the 151P3D4 protein, where the status of

CC a cell that expresses the 151P3D4 protein is modulated. The novel

CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting

CC a humoral or cellular immune response. The 151P3D4 genes and proteins

CC are also useful for diagnosing, prognosing, preventing or treating

CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or

CC bronchial cancer, breast cancer or carcinoma. This sequence represents a

CC 151P3D4 related peptide of the invention

XX

SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9

Db 2 FPDKKHKL 9

RESULT 42

ABJ41450

ID ABJ41450 standard; peptide; 9 AA.

XX

AC ABJ41450;

XX

DT 17-OCT-2003 (first entry)

XX

DE 151P3D4 cancer gene related peptide #2077.

XX

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;

KW bronchial; breast; carcinoma.

XX

OS Unidentified.

XX

PN WO200283860-A2.

XX

PD 24-OCT-2002.

XX

PF 09-APR-2002; 2002WO-US011644.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

PI Morrison RK, Ge W, Jakobovits A;

XX

DR WPI; 2003-167091/16.

XX

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

PT cellular immune response, or for diagnosing, prognosing, preventing or

PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer

PT or carcinoma.

XX

PS Claim 13; Page 147; 426pp; English.

XX

CC The invention relates to a novel composition comprising a substance that

CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or

CC a molecule that is modulated by the 151P3D4 protein, where the status of

CC a cell that expresses the 151P3D4 protein is modulated. The novel

CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting

CC a humoral or cellular immune response. The 151P3D4 genes and proteins

CC are also useful for diagnosing, prognosing, preventing or treating

CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or

CC bronchial cancer, breast cancer or carcinoma. This sequence represents a

CC 151P3D4 related peptide of the invention

XX

SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9

Db 1 FPDKKHKL 8

RESULT 43

ABJ46607

ID ABJ46607 standard; peptide; 9 AA.

XX

AC ABJ46607;

XX

DT 16-OCT-2003 (first entry)

XX

DE 151P3D4 cancer gene related HLA peptide #4427.

XX

KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;

KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.

XX

OS Homo sapiens.

XX

PN WO200283860-A2.

XX

PD 24-OCT-2002.

XX

PF 09-APR-2002; 2002WO-US011644.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;

PI Morrison RK, Ge W, Jakobovits A;

XX

DR WPI; 2003-167091/16.

XX

PT New 151P3D4 proteins and genes, useful for eliciting a humoral or

PT cellular immune response, or for diagnosing, prognosing, preventing or

PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer

PT or carcinoma.

XX

PS Claim 13; Page 201; 426pp; English.

XX

CC The invention relates to a novel composition comprising a substance that

CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or

CC a molecule that is modulated by the 151P3D4 protein, where the status of

CC a cell that expresses the 151P3D4 protein is modulated. The novel

CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting

CC a humoral or cellular immune response. The 151P3D4 genes and proteins

CC are also useful for diagnosing, prognosing, preventing or treating

CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or

CC bronchial cancer, breast cancer or carcinoma. This sequence represents a

CC human leukocyte antigen peptide relating to the 151P3D4 composition of

CC the invention

XX

SQ Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9

Db 1 FPDKKHKL 8

RESULT 44
ABJ40977
ID ABJ40977 standard; peptide; 9 AA.
XX
AC ABJ40977;
XX
DT 17-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related peptide #1604.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma.
XX
OS Unidentified.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 143; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC 151P3D4 related peptide of the invention
XX
SQ Sequence 9 AA;
Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 FPDENFKL 9
|||: ||
Db 2 FPDKKHKL 9
RESULT 45
ABJ49160
ID ABJ49160 standard; peptide; 9 AA.
XX
AC ABJ49160;
XX
DT 16-OCT-2003 (first entry)
XX
DE 151P3D4 cancer gene related HLA peptide #6980.
XX
KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO200283860-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US011644.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI Morrison RK, Ge W, Jakobovits A;
XX
DR WPI; 2003-167091/16.
XX
PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT cellular immune response, or for diagnosing, prognosing, preventing or
PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT or carcinoma.
XX
PS Claim 13; Page 225; 426pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC a molecule that is modulated by the 151P3D4 protein, where the status of
CC a cell that expresses the 151P3D4 protein is modulated. The novel
CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC a humoral or cellular immune response. The 151P3D4 genes and proteins
CC are also useful for diagnosing, prognosing, preventing or treating
CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC human leukocyte antigen peptide relating to the 151P3D4 composition of
CC the invention
XX
SQ Sequence 9 AA;
Query Match 56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 FPDENFKL 9
|||: ||
Db 2 FPDKKHKL 9

Search completed: August 30, 2004, 10:49:35
Job time : 15.4088 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	53.4	9	4 Q9H326	Q9h326 homo sapien
2	26	44.8	10	11 Q9QVE9	Q9qve9 mus sp. pro
3	24	41.4	9	13 Q9PRJ4	Q9prj4 lepisosteus
4	24	41.4	12	15 Q12090	Q12090 caprine art
5	24	41.4	12	15 Q12094	Q12094 caprine art
6	24	41.4	12	15 Q12114	Q12114 caprine art
7	24	41.4	12	15 Q12082	Q12082 caprine art
8	24	41.4	12	15 Q12106	Q12106 caprine art
9	24	41.4	12	15 Q12092	Q12092 caprine art
10	24	41.4	12	15 Q12108	Q12108 caprine art
11	24	41.4	12	15 Q12074	Q12074 caprine art
12	24	41.4	12	15 Q12116	Q12116 caprine art
13	24	41.4	12	15 Q12118	Q12118 caprine art
14	24	41.4	12	15 Q12110	Q12110 caprine art
15	24	41.4	12	15 Q12112	Q12112 caprine art
16	24	41.4	12	15 Q12076	Q12076 caprine art

17	24	41.4	12	15	Q12088	Q12088 caprine art
18	24	41.4	12	15	Q12078	Q12078 caprine art
19	24	41.4	12	15	Q12080	Q12080 caprine art
20	24	41.4	12	15	Q12084	Q12084 caprine art
21	24	41.4	12	15	Q12086	Q12086 caprine art
22	22	37.9	12	7	Q77915	Q77915 oreochromis
23	21	36.2	8	6	Q9TRY3	Q9try3 sus sp. ins
24	21	36.2	12	10	Q93YC8	Q93yc8 nicotiana t
25	21	36.2	14	2	Q9R5P6	Q9r5p6 legionella
26	21	36.2	14	5	Q18502	Q18502 schistosoma
27	20	34.5	14	7	Q8MH06	Q8mh06 homo sapien
28	20	34.5	14	7	Q8MH35	Q8mh35 homo sapien
29	20	34.5	14	7	Q8MH39	Q8mh39 homo sapien
30	20	34.5	14	7	Q8MH18	Q8mh18 homo sapien
31	20	34.5	14	7	Q8MH55	Q8mh55 homo sapien
32	20	34.5	14	7	Q8MH40	Q8mh40 homo sapien
33	20	34.5	14	7	Q8MH07	Q8mh07 homo sapien
34	20	34.5	14	7	Q8MH04	Q8mh04 homo sapien
35	20	34.5	14	7	Q8MH52	Q8mh52 homo sapien
36	20	34.5	14	7	Q8MH26	Q8mh26 homo sapien
37	20	34.5	14	7	Q8MH53	Q8mh53 homo sapien
38	20	34.5	14	7	Q8MH20	Q8mh20 homo sapien
39	20	34.5	14	7	Q8MH27	Q8mh27 homo sapien
40	20	34.5	14	7	Q8MH05	Q8mh05 homo sapien
41	20	34.5	14	7	Q8MH16	Q8mh16 homo sapien
42	20	34.5	14	7	Q8MH38	Q8mh38 homo sapien
43	20	34.5	14	7	Q8MH56	Q8mh56 homo sapien
44	20	34.5	14	7	Q8MH14	Q8mh14 homo sapien
45	20	34.5	14	7	Q8MH31	Q8mh31 homo sapien

ALIGNMENTS

RESULT 1
Q9H326
ID Q9H326 PRELIMINARY; PRT; 9 AA.
AC Q9H326;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit
DE (Fragment).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-
dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 53.4%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWVS 8
||| |:
Db 3 GPAWIS 8

RESULT 2
Q9QVE9
ID Q9QVE9 PRELIMINARY; PRT; 10 AA.
AC Q9QVE9;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)

```
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/11 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1029 MW; FCAD2DD8676866D1 CRC64;

Query Match 44.8%; Score 26; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPG 5
Db | |||
3 HQGPG 7

RESULT 3
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (Long-nosed gar), and
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 41.4%; Score 24; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db | |||
3 PGW 5

RESULT 4
O12090 PRELIMINARY; PRT; 12 AA.
AC O12090;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/11 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1029 MW; FCAD2DD8676866D1 CRC64;

Query Match 44.8%; Score 26; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPG 5
Db | |||
3 HQGPG 7

RESULT 3
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (Long-nosed gar), and
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus.
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 41.4%; Score 24; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db | |||
3 PGW 5

RESULT 4
O12090 PRELIMINARY; PRT; 12 AA.
AC O12090;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
```

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RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db | |||
8 PGW 10

RESULT 5
O12094 PRELIMINARY; PRT; 12 AA.
AC O12094;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81438; AAB60830.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db | |||
8 PGW 10

RESULT 6
O12114 PRELIMINARY; PRT; 12 AA.
AC O12114;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
RT to A substitutions.";
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RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81448; AAB60850.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 7
O12082 PRELIMINARY; PRT; 12 AA.
ID O12082
AC O12082;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81432; AAB60818.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 8
O12106 PRELIMINARY; PRT; 12 AA.
ID O12106
AC O12106;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81444; AAB60842.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 9
O12092 PRELIMINARY; PRT; 12 AA.
ID O12092
AC O12092;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81437; AAB60828.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 10
O12108 PRELIMINARY; PRT; 12 AA.
ID O12108
AC O12108;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81445; AAB60844.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.

```
FT NON TER 1 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 11
O12074 PRELIMINARY; PRT; 12 AA.
AC O12074;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81428; AAB60810.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 12
O12116 PRELIMINARY; PRT; 12 AA.
AC O12116;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81449; AAB60852.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
```

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Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 13
O12118 PRELIMINARY; PRT; 12 AA.
AC O12118;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81450; AAB60854.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 14
O12110 PRELIMINARY; PRT; 12 AA.
AC O12110;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81446; AAB60846.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10
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```
QY          4 PGW 6
Db          8 PGW 10

RESULT 15
O12112      PRELIMINARY;      PRT;      12 AA.
ID O12112
AC O12112;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81447; AAB60848.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match          41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 PGW 6
Db          8 PGW 10

RESULT 16
O12076      PRELIMINARY;      PRT;      12 AA.
ID O12076
AC O12076;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81429; AAB60812.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match          41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 PGW 6
Db          8 PGW 10

RESULT 17
O12088      PRELIMINARY;      PRT;      12 AA.
ID O12088
AC O12088;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81435; AAB60824.1; -.
FT NON TER 1
SQ SEQUENCE 12 AA; 1279 MW; 4B90BBB1E8644EB7 CRC64;

Query Match          41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 PGW 6
Db          8 PGW 10

RESULT 18
O12078      PRELIMINARY;      PRT;      12 AA.
ID O12078
AC O12078;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81430; AAB60814.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match          41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 PGW 6
Db          8 PGW 10

RESULT 19
O12080      PRELIMINARY;      PRT;      12 AA.
ID O12080
AC O12080;
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DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81431; AAB60816.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 20
O12084 PRELIMINARY; PRT; 12 AA.
AC O12084;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81433; AAB60820.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 21
O12086 PRELIMINARY; PRT; 12 AA.
ID O12086
AC O12086;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
```

```
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81434; AAB60822.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 8 PGW 10

RESULT 22
O77915 PRELIMINARY; PRT; 12 AA.
ID O77915
AC O77915;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050028; AAC41367.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1426 MW; 9D2F47DB7A787045 CRC64;

Query Match 37.9%; Score 22; DB 7; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 GWVSM 9
Db .7 GWIAV 11

RESULT 23
Q9TRY3 PRELIMINARY; PRT; 8 AA.
ID Q9TRY3
AC Q9TRY3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 36.2%; Score 21; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 2 GPCW 5

RESULT 24
Q93YC8 PRELIMINARY; PRT; 12 AA.
ID Q93YC8;
AC Q93YC8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coat protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Winden J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027532; PubMed=10557305;
RA Jakowitsch J., Mette M.F., van der Winden J., Matzke M.A.,
RA Matzke A.J.;
RT "Integrated pararetroviral sequences define a unique class of
RT dispersed repetitive DNA in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).
DR EMBL; AJ414170; CAC88799.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1402 MW; 89226B3A0351E321 CRC64;

Query Match 36.2%; Score 21; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYG 3
Db 7 HYG 9

RESULT 25
Q9R5P6 PRELIMINARY; PRT; 14 AA.
ID Q9R5P6
AC Q9R5P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major outer membrane protein 31 kDa subunit, MOMP 31 kDa subunit
DE (Fragment).
```

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OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RX MEDLINE=92121130; PubMed=1310095;
RA Hoffman P.S., Seyer J.H., Butler C.A.;
RT "Molecular characterization of the 28- and 31-kilodalton subunits of
RT the Legionella pneumophila major outer membrane protein.";
RL J. Bacteriol. 174:908-913(1992).
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1490 MW; 3541B0FB1AF55F48 CRC64;

Query Match 36.2%; Score 21; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 1 GPCW 4

RESULT 26
O18502 PRELIMINARY; PRT; 14 AA.
ID O18502
AC O18502;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lysophospholipase homolog (Fragment).
GN SMLPLH.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Egyptian;
RX MEDLINE=99011094; PubMed=9797070;
RA Hamdan F.F., Ribeiro P.;
RT "Cloning and sequence analysis of a lysophospholipase homologue from
RT Schistosoma mansoni.";
RL Parasitol. Res. 84:839-842(1998).
DR EMBL; AF006679; AAC62255.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 48B847C2E5D89177 CRC64;

Query Match 36.2%; Score 21; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 11 GPCW 14

RESULT 27
Q8MH06 PRELIMINARY; PRT; 14 AA.
ID Q8MH06
AC Q8MH06;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```



```
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AF533934; AAM94848.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 28
Q8MH35 PRELIMINARY; PRT; 14 AA.
AC Q8MH35;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AF533905; AAM94819.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 29
Q8MH39 PRELIMINARY; PRT; 14 AA.
AC Q8MH39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AF533901; AAM94815.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 30
Q8MH18 PRELIMINARY; PRT; 14 AA.
AC Q8MH18;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AF533922; AAM94836.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 31
Q8MH55 PRELIMINARY; PRT; 14 AA.
AC Q8MH55;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515808; AAM74915.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 32
Q8MH40
ID Q8MH40 PRELIMINARY; PRT; 14 AA.
AC Q8MH40;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533900; AAM94814.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 33
Q8MH07
ID Q8MH07 PRELIMINARY; PRT; 14 AA.
AC Q8MH07;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
```

```
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533933; AAM94847.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13
```

```
RESULT 34
Q8MH04
ID Q8MH04 PRELIMINARY; PRT; 14 AA.
AC Q8MH04;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533936; AAM94850.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13
```

```
RESULT 35
Q8MH52
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ID Q8MH52 PRELIMINARY; PRT; 14 AA.
AC Q8MH52;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515811; AAM74918.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 36
Q8MH26 PRELIMINARY; PRT; 14 AA.
ID Q8MH26
AC Q8MH26;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533914; AAM94828.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 37
Q8MH53 PRELIMINARY; PRT; 14 AA.
ID Q8MH53
AC Q8MH53;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515810; AAM74917.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 38
Q8MH20 PRELIMINARY; PRT; 14 AA.
ID Q8MH20
AC Q8MH20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533920; AAM94834.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 39
Q8MH27 PRELIMINARY; PRT; 14 AA.
ID Q8MH27
AC Q8MH27;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533913; AAM94827.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 40
Q8MH05
ID Q8MH05 PRELIMINARY; PRT; 14 AA.
AC Q8MH05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533935; AAM94849.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 41
Q8MH05
ID Q8MH05 PRELIMINARY; PRT; 14 AA.
AC Q8MH05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533935; AAM94849.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13
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Q8MH16
ID Q8MH16 PRELIMINARY; PRT; 14 AA.
AC Q8MH16;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533924; AAM94838.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 42
Q8MH38
ID Q8MH38 PRELIMINARY; PRT; 14 AA.
AC Q8MH38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533902; AAM94816.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13
```

Db 10 HQGP 13

RESULT 43
Q8MH56 PRELIMINARY; PRT; 14 AA.
ID Q8MH56
AC Q8MH56;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515807; AAM74914.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 44
Q8MH14 PRELIMINARY; PRT; 14 AA.
ID Q8MH14
AC Q8MH14;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533926; AAM94840.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

RESULT 45

Q8MH31 PRELIMINARY; PRT; 14 AA.
ID Q8MH31
AC Q8MH31;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533909; AAM94823.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
Db 10 HQGP 13

Search completed: August 30, 2004, 10:55:26
Job time : 8.66554 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.55068 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	51.7	11	CA31_LITCI	P82089 litoria cit
2	29	50.0	11	CA32_LITCI	P82090 litoria cit
3	28	48.3	8	RPCH_PANBO	P08939 pandalus bo
4	28	48.3	10	HTF_NAUCI	P10939 nauphoeta c
5	26	44.8	10	GONL_SQUAC	P27429 squalus aca
6	25	43.1	8	AKH_MELML	P25423 melolontha
7	25	43.1	8	AKH_TABAT	P14595 tabanus atr
8	25	43.1	10	GON2_CHICK	P37043 gallus gall
9	25	43.1	10	GON3_ONCKE	P20367 oncorhynch
10	25	43.1	10	HTF_TABAT	P14596 tabanus atr
11	24	41.4	10	BRK_ONCMY	Q9prz1 oncorhynch
12	23.5	40.5	12	RFL_CONSP	P58805 conus spuri
13	23	39.7	10	COXO_RAT	P80432 rattus norv
14	23	39.7	10	COXO_THUOB	P80982 thunnus obe
15	23	39.7	11	CORZ_PERAM	P11496 periplaneta
16	22	37.9	8	HTF1_PERAM	P04548 periplaneta
17	22	37.9	8	HTF_TENMO	P25419 tenebrio mo
18	22	37.9	13	BOML_PSEGU	P42991 pseudophryn
19	21	36.2	10	GON1_PETMA	P04378 petromyzon
20	20	34.5	8	AKHG_GRYBI	P14086 gryllus bim
21	20	34.5	8	AKH_LIBAU	P25418 libellula a
22	20	34.5	10	HTF1_ROMMI	P18110 romalea mic
23	20	34.5	11	OAIIF_SARBU	P83518 sarcophaga
24	20	34.5	12	NUDM_CANFA	P54713 canis famil
25	19	32.8	8	HTF2_PERAM	P04549 periplaneta
26	19	32.8	10	HTF2_CARMO	P11385 carausius m
27	19	32.8	10	HTF_HELZE	P16353 heliothis z
28	18	31.0	8	CKKN_MACEU	P30369 macropus eu
29	18	31.0	10	CAER_LITXA	P56264 litoria xan
30	18	31.0	10	GON3_PETMA	P30948 petromyzon
31	18	31.0	14	IF2G_RAT	P81795 rattus norv
32	18	31.0	14	MCRZ_METTM	P58816 methanobact
33	17	29.3	8	ALLI_CYDPO	P82152 cydia pomon

34	17	29.3	8	1	UF06_MOUSE	P38644 mus musculu
35	17	29.3	9	1	LMIP_LOCMI	P31799 locusta mig
36	17	29.3	10	1	BPP_VIPAS	P31351 vipera aspi
37	17	29.3	10	1	CA12_LITCI	P82086 litoria cit
38	17	29.3	11	1	RANC_RANPI	P08951 rana pipien
39	17	29.3	13	1	BPP1_BOTJA	P01020 bothrops ja
40	17	29.3	13	1	UP71_LITEW	P82050 litoria ewi
41	17	29.3	14	1	LPW_CITFR	P03056 citrobacter
42	17	29.3	14	1	LPW_ECOLI	P03053 escherichia
43	17	29.3	14	1	LPW_SALTY	P03054 salmonella
44	16	27.6	8	1	LCK2_LEUMA	P21141 leucophaea
45	16	27.6	9	1	BS43_SERPL	P83375 serratia pl

ALIGNMENTS

RESULT 1
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being sulfated.
CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;
Query Match 51.7%; Score 30; DB 1; Length 11;
Best Local Similarity 56.7%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGPGWV 7
|||
Db 4 YGTGWM 9
RESULT 2
CA32_LITCI
ID CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 50.0%; Score 29; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 27;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
DB : : : :
4 YGTGW 8

RESULT 3
RPCH PANBO STANDARD; PRT; 8 AA.
ID RPCH PANBO
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
OC Pandalidae; Pandalus.
OX NCBI_TaxID=6703;
RN [1]
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=4433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
RT Pandanus borealis.";
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -!- FUNCTION: This hormone adapts the animal to light backgrounds by
CC stimulating concentration of the pigment of its red body-
CC chromatophores.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro; IPR002047; AKH.
DR PIR; A61348; A61348.
DR PROSITE; PS00256; AKH; 1.
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 48.3%; Score 28; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
DB : : : :
3 NFSPGW 8

RESULT 4
HTF NAUCI STANDARD; PRT; 10 AA.
ID HTF NAUCI
AC P10939;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Leucophaea maderae (Madeira cockroach),
OS Blattella germanica (German cockroach), and
OS Gromphadorina portentosa (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Nauphoeta.
OX NCBI_TaxID=6990, 6988, 6973, 36953;
RN [1]
RP SEQUENCE.
RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
RX MEDLINE=87100208; PubMed=3801028;
RA Gaede G., Rinehart K.L. Jr.;
RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
RT corpus cardiacum of the cockroach, Nauphoeta cinerea.";
RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
RN [2]
RP SEQUENCE.
RC SPECIES=L.maderae, G.portentosa, and B.germanica;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP SEQUENCE.
RC SPECIES=B.germanica;
RX MEDLINE=91179584; PubMed=2080017;
RA Veenstra J.A., Camps F.;
RT "Structure of the hypertrehalosemic neuropeptide of the German
RT cockroach, Blattella germanica.";
RL Neuropeptides 15:107-109(1990).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A26381; A26381.
DR PIR; A60421; A60421.
DR PIR; S08997; S08997.
DR PIR; S08998; S08998.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;

Query Match 48.3%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
DB : : : :
3 NFSPGW 8

RESULT 5

GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH) (Luliberin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
RT dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GNRH family.
DR PIR; A46030; A46030.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 44.8%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7

|:|:

Db 2 HWSHGWL 8

RESULT 6

AKH_MELML STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorosus (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
OC Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; PubMed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetic
RT hormone/red-pigment-concentrating hormone peptide family isolated and
RT sequenced from two beetle species.";
RL Biochem. J. 275:671-677(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX MEDLINE=92265187; PubMed=1586453;

RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT "Primary structures of neuropeptides isolated from the corpora
RT cardiaca of various cetonid beetle species determined by
RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT spectrometry.";
RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A58641; A58641.
DR PIR; S15422; S15422.
DR PIR; S21663; S21663.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 43.1%; Score 25; DB 1; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6

:| |

Db 3 NYS PDW 8

RESULT 7

AKH_TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A33995; A33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 43.1%; Score 25; DB 1; Length 8;

Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      2 YGPGW 6
      : |||
Db      4 FTPGW 8

RESULT 8
GON2_CHICK
ID  GON2_CHICK  STANDARD;  PRT;  10 AA.
AC  P37043; P20408; P81750;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Gonadoliberein II (Gonadotropin-releasing hormone II) (GnRH-II)
DE  (LH-RH II) (Luliberin II).
OS  Gallus gallus (Chicken),
OS  Alligator mississippiensis (American alligator),
OS  Squalus acanthias (Spiny dogfish),
OS  Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and
OS  Clupea pallasii (Pacific herring).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Gallus.
OX  NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=Chicken; TISSUE=Hypothalamus;
RX  MEDLINE=84222059; PubMed=6427779;
RA  Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA  Matsuo H.;
RT  "Identification of the second gonadotropin-releasing hormone in
RT  chicken hypothalamus: evidence that gonadotropin secretion is
RT  probably controlled by two distinct gonadotropin-releasing hormones
RT  in avian species.";
RL  Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN  [2]
RP  SEQUENCE.
RC  SPECIES=A.mississippiensis; TISSUE=Brain;
RX  MEDLINE=91352338; PubMed=1882082;
RA  Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA  Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT  "Primary structure of two forms of gonadotropin-releasing hormone
RT  from brains of the American alligator (Alligator mississippiensis).";
RL  Regul. Pept. 33:105-116(1991).
RN  [3]
RP  SEQUENCE.
RC  SPECIES=S.acanthias; TISSUE=Brain;
RX  MEDLINE=92335300; PubMed=1631133;
RA  Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA  Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT  "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
RT  dogfish brain provides insight into GnRH evolution.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
RN  [4]
RP  SEQUENCE.
RC  SPECIES=H.colliei; TISSUE=Brain;
RX  MEDLINE=91340067; PubMed=1678723;
RA  Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA  Lee T.;
RT  "Primary structure of gonadotropin-releasing hormone from the brain
RT  of a holoccephalan (ratfish: Hydrolagus colliei).";
RL  Gen. Comp. Endocrinol. 82:152-161(1991).
RN  [5]
RP  SEQUENCE, AND FUNCTION.
RC  SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX  MEDLINE=20114351; PubMed=10650929;
RA  Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA  Chang J.P., Rivier J.E., Sherwood N.M.;
RT  "Primary structure and function of three gonadotropin-releasing
RT  hormones, including a novel form, from an ancient teleost, herring.";
RL  Endocrinology 141:505-512(2000).
CC  -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the GnRH family.

QY      1 HYGPGW 6
      : |||
Db      2 HWSHGW 7

Query Match      43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
GON3_ONCKE
ID  GON3_ONCKE  STANDARD;  PRT;  10 AA.
AC  P20367; P81751;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Gonadoliberein III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
DE  RH III) (Luliberin III).
GN  GNRH3.
OS  Oncorhynchus keta (Chum salmon), and
OS  Clupea pallasii (Pacific herring).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX  NCBI_TaxID=8018, 30724;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=O.keta;
RX  MEDLINE=83195140; PubMed=6341999;
RA  Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT  "Characterization of a teleost gonadotropin-releasing hormone.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN  [2]
RP  SEQUENCE, AND FUNCTION.
RC  SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX  MEDLINE=20114351; PubMed=10650929;
RA  Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA  Chang J.P., Rivier J.E., Sherwood N.M.;
RT  "Primary structure and function of three gonadotropin-releasing
RT  hormones, including a novel form, from an ancient teleost, herring.";
RL  Endocrinology 141:505-512(2000).
CC  -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC  the secretion of both luteinizing and follicle-stimulating
CC  hormones.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the GnRH family.

QY      1 HYGPGW 7
      : |||
Db      2 HWSYGWL 8

Query Match      43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 10
HTF TABAT
ID HTF TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II) (DCC II).
DE Tabanus atratus (Horse fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
hypotrehalosemic activity isolated from the corpora cardiaca of horse
flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;
Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGPGW 6
Db : |||
4 FTGPGW 8
RESULT 11
BRK ONCMY
ID BRK ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the bradykinin family.

DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;
Query Match 41.4%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db |||
4 PGW 6
RESULT 12
RF1 CONSP STANDARD; PRT; 12 AA.
AC P58805;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conorfamide-Srl.
OS Conus spurius (Alphabet cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=192919;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RX TISSUE=Venom;
MEDLINE=21605839; PubMed=11738233;
RA Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA Olivera B.M., Heimer de la Cotera E.P.;
RT "Conorfamide, a Conus venom peptide belonging to the RFamide family of
neuropeptides.";
RL Toxicon 40:401-407(2002).
CC -!- FUNCTION: Causes hyperactivity in mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KW Neurotoxin; Toxin; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;
Query Match 40.5%; Score 23.5; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 3 GP-GWV 7
Db |||
1 GPMGWV 6
RESULT 13
COXO RAT
ID COXO RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
(VIIIA) (Fragment).
DE COX7C OR COX7C1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX STRAIN=Wistar; TISSUE=Heart, and Liver;
MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S65388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 39.7%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
DB 2 HYEFGPG 8

RESULT 14
COXO THUOB STANDARD; PRT; 10 AA.
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F., Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S77990; S77990.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 39.7%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
DB 2 HYEFGPG 8

RESULT 15
CORZ PERAM STANDARD; PRT; 11 AA.
ID CORZ PERAM
AC P11436;
DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.";
RL FEBS Lett. 250:231-234(1989).
CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 39.7%; Score 23; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.9e+02;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
DB 5 YSRGWTN 11

RESULT 16
HTF1 PERAM STANDARD; PRT; 8 AA.
ID HTF1 PERAM
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I) (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E., Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A., Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.declineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;

RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 RL beetle and the American cockroach are identical.";
 RN Peptides 10:1287-1289(1989).
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is
 CC the major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A05169; A05169.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 37.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPGW 6
 Db ::|||
 3 NFSPNW 8
 RESULT 17
 HTF TENMO STANDARD; PRT; 8 AA.
 ID P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic factor (HOTH) (Hypertrehalosemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=T.molitor, and Z.rugipes;
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 RT tenebrionid beetles; a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990).
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
 DR PIR; A43976; A43976.
 DR PIR; B43976; B43976.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;
 Query Match 37.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPGW 6
 Db ::|||
 3 NFSPNW 8
 RESULT 18
 BOML PSEGU STANDARD; PRT; 13 AA.
 ID P42991;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bombesin-like peptide L (PG-L).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
 CC family.
 DR PIR; A60409; A60409.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;
 Query Match 37.9%; Score 22; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.1e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GPGW 6
 Db ||||
 4 GPGW 7
 RESULT 19
 GONI PETMA STANDARD; PRT; 10 AA.
 ID GONI PETMA
 AC P04378;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I)
 DE (Luliberin I).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey
brain.";
RL J. Biol. Chem. 261:4812-4819(1986).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A01412; RHLMSG.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 36.2%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db |||
2 HYSLEW 7

RESULT 20
AKHG GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;
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Query Match 34.5%; Score 20; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db ::||
3 NFSTGW 8

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db ::||
3 NFPSW 8

RESULT 22
HTF1 ROMMI STANDARD; PRT; 10 AA.
ID HTF1_ROMMI STANDARD; PRT; 10 AA.
AC P18110;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehalosaemic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
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RT the lubber grasshopper, Romalea microptera." ;
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro: IPR02047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 8.6e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db ::|||
3 NFTPW 8

RESULT 23
OAIIF_SARBU STANDARD; PRT; 11 AA.
AC P83518;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]

SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=2272747; PubMed=12383874;
RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L., De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme substrate from vitellogenic ovaries of Neobellieria bullata.";
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYSM 9
Db ::|||
8 WISL 11

RESULT 24
NUDM_CANFA STANDARD; PRT; 12 AA.
AC P54713;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).
GN NDUFAL0.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 FAD per subunit.
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits. This a component of the hydrophobic protein fraction.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
DR HSC-2DPAGE; P54713; DOG.
KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGP 4
Db ::|||
3 YGP 5

RESULT 25
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2) (PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E., Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A., Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).

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RT [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B49960; B49960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 32.8%; Score 19; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YCPGW 6
Db : | |
4 FTPNW 8

RESULT 26
HTF2 CARMO
ID HTF2 CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
corpus cardiaca of the Indian stick insect, Carausius morosus,
determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from

the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
a stick insect corpus cardiaca.";
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; JCI416; JCI416.
DR PIR; S09138; S09138.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 32.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YCPGW 6
Db : | |
4 FTPNW 8

RESULT 27
HTF HELZE
ID HTF HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (HeZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
Heliothis zea with hypertrehalosemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A31571; A31571.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

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Query Match      32.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 YGPGW 6
Db      :
        4 FSSGW 8

RESULT 28
CCKN_MACEU      STANDARD;      PRT;      8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M.eugenii, and D.viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match      31.0%; Score 18; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 GWV 7
Db      :
        4 GWM 6

RESULT 29
CAER_LITXA      STANDARD;      PRT;      10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;

Query Match      32.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 YGPGW 6
Db      :
        4 FSSGW 8

RESULT 28
CCKN_MACEU      STANDARD;      PRT;      8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M.eugenii, and D.viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match      31.0%; Score 18; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 GWV 7
Db      :
        4 GWM 6

RESULT 29
CAER_LITXA      STANDARD;      PRT;      10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;

Query Match      31.0%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HYGPGW 6
Db      :
        2 HWSHDW 7

RESULT 31
IF2G_RAT
ID IF2G_RAT
AC P81795;

Query Match      31.0%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HYGPGW 6
Db      :
        2 HWSHDW 7

RESULT 31
IF2G_RAT
ID IF2G_RAT
AC P81795;
```

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic
DE translation initiation factor 2 gamma subunit) (eIF-2-gamma) (PP42)
DE (Fragment).
GN EIF2S3 OR EIF2G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96374441; PubMed=8780732;
RA Gil C., Plana M., Riera M., Itarte E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eIF-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -!- FUNCTION: eIF-2 functions in the early steps of protein synthesis
CC by forming a ternary complex with GTP and initiator tRNA. This
CC complex binds to a 40S ribosomal subunit, followed by mRNA binding
CC to form a 43S preinitiation complex. Junction of the 60S ribosomal
CC subunit to form the 80S initiation complex is preceded by
CC hydrolysis of the GTP bound to eIF-2 and release of an eIF-2-GDP
CC binary complex. In order for eIF-2 to recycle and catalyze another
CC round of initiation, the GDP bound to eIF-2 must exchange with GTP
CC by way of a reaction catalyzed by eIF-2b.
CC -!- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
CC chain.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EIF2G subfamily.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON TER 1 1
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1511 MW; D86EDA955ABEFA12 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PGWVS 8
DB 9 PGIVS 13

RESULT 32
MCRZ METTM STANDARD; PRT; 14 AA.
AC P58816;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
DE gamma) (Fragment).
GN MRTG.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and delta H.";
RL Eur. J. Biochem. 194:871-877(1990).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.

CC Coenzyme F430 is a yellow nickel porphyrinoid.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CC CONTAINS MOSTLY MCR I.
DR PIR; E69017; E69017.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT INIT MET 0
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1557 MW; 97E9439C4223B871 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPG 5
DB 6 YTPG 9

RESULT 33
ALL1 CYDPO STANDARD; PRT; 8 AA.
ID ALL1 CYDPO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricodea; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8
FT SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPG 5
DB 3 HYNFG 7

RESULT 34
UF06 MOUSE STANDARD; PRT; 8 AA.
ID UF06 MOUSE
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 kDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPG 5
Db 1 HSEPG 5

RESULT 35

LMIP_LOCFI ID LMIP LOCFI STANDARD; PRT; 9 AA.
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyo inhibiting peptide (LOM-MIP).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyo inhibiting
RT peptide (LOM-MIP), a novel biologically active neuropeptide from
RT Locusta migratoria.";
RL Regul. Pept. 36:111-119(1991).
CC -!- FUNCTION: Suppresses spontaneous contractions of the hindgut and
CC oviduct.
CC -!- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters
CC in the suboesophageal ganglion.
CC PIR; A60065; AKLQIM.
DR Amidation; Neuropeptide.
KW MOD RES 9
FT SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
Db 8 GW 9

RESULT 36

BPP_VIPAS ID BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
Db 2 GW 3

RESULT 37

CAL2_LITCI ID CAL2 LITCI STANDARD; PRT; 10 AA.
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770, 30345;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
RC SPECIES=L.citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendipherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10.";
RL Eur. J. Biochem. 267:269-275(2000).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1
FT MOD_RES 4
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;

Query Match 29.3%; Score 17; DB 1; Length 10;

```
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GW 6
Db      6 GW 7

RESULT 38
RANC_RANPI      STANDARD;      PRT;      11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
    family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD RES      11
SQ SEQUENCE      11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match      29.3%; Score 17; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 PGWVS 8
Db      3 PQWAT 7

RESULT 39
BPPI_BOTJA      STANDARD;      PRT;      13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
    enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
    Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
    jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
```

```
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
    peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
    angiotensin-converting enzyme and enhances the action of
    bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES      1
SQ SEQUENCE      13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match      29.3%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GW 6
Db      3 GW 4

RESULT 40
UP71_LITEW      STANDARD;      PRT;      13 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 7.1 [Contains: Uperin 7.1.1].
OS Litoria ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104896;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combinaon of peptides from the skin glands of Ewing's
    tree frog, Litoria ewingi. Sequence determination and antimicrobial
    activity.";
RL Aust. J. Chem. 50:889-894(1997).
CC -!- FUNCTION: Uperin 7.1 shows antibacterial activity against L.lactis
    and S.uberis. Uperin 7.1.1 is inactive.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.
CC -!- MASS SPECTROMETRY: MW=1184; METHOD=FAB; RANGE=3-13.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT PEPTIDE      1 13 UPERIN 7.1.
FT PEPTIDE      3 13 UPERIN 7.1.1.
FT MOD RES      13
SQ SEQUENCE      13 AA; 1429 MW; DE17C7204CCAE322 CRC64;

Query Match      29.3%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GW 6
Db      1 GW 2

RESULT 41
LPW_CITFR      STANDARD;      PRT;      14 AA.
ID LPW_CITFR
AC P03056;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;
RT "Evolutionary divergence of the Citrobacter freundii tryptophan
operon regulatory region: comparison with other enteric bacteria.";
RL J. Bacteriol. 152:57-62(1982).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC -----
CC EMBL; J01557; -; NOT_ANNOTATED_CDS.
DR PIR; A03592; LFEBCW.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 14 AA; 1720 MW; 5B792A473E8048E7 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
Db 9 GW 10

RESULT 42
LPW_ECOLI STANDARD; PRT; 14 AA.
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPEE OR B1265 OR C5494 OR Z2545 OR ECS1837 OR SF1268 OR
GN S4805.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA Horowitz H., van Cleemput M., Wu A.M.;
RT "The complete nucleotide sequence of the tryptophan operon of
Escherichia coli.";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
Escherichia coli.";

RL J. Mol. Biol. 103:351-381(1976).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
secondary structure involving the tryptophan codon region.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;

RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
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DR EMBL; J01714; AAA57296.1; -.
DR EMBL; A04494; CAA00361.1; -.
DR EMBL; AE000224; AAC74347.1; -.
DR EMBL; AE016760; AAN80196.1; -.
DR EMBL; AE005380; AAG56550.1; -.
DR EMBL; AP002556; BAB35260.1; -.
DR EMBL; AE015153; AAN42881.1; -.
DR EMBL; AE016982; AAP16766.1; -.
DR PIR; A03589; LFECW.
DR PIR; B85761; B85761.
DR PIR; E90858; E90858.
DR EcoGene; EG11274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
Db 9 GW 10

RESULT 43
LPW SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPEE OR STM1722.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=78196931; PubMed=3511195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
RT regions of the tryptophan operons of Escherichia coli and Salmonella
RT typhimurium.";
RL J. Mol. Biol. 121:193-217(1978).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
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DR EMBL; M24960; -; NOT ANNOTATED CDS.
DR EMBL; AE008776; AAL20640.1; -.
DR PIR; A03590; LFEBWT.
DR StyGene; SG10400; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
Db 9 GW 10

RESULT 44
LCK2 LEUMA STANDARD; PRT; 8 AA.
ID LCK2 LEUMA
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AMIDATION.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 27.6%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PGWVS 8
Db 2 PGFSS 6

RESULT 45
BS43 SERPL STANDARD; PRT; 9 AA.
ID BS43 SERPL
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.

OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against *Erwinia amylovora*, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC *E. amylovora*.
KW Antibiotic; Bacteriocin.
FT NON TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 27.6%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYG 3
|:|
Db 3 HHG 5

Search completed: August 30, 2004, 10:50:23
Job time : 1.55068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HVGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	48.3	8	2 A61348	red pigment-concen
2	28	48.3	10	2 A60421	hypertrehalosemic
3	28	48.3	10	2 S08997	hypertrehalosemic
4	28	48.3	10	2 S08998	hypertrehalosemic
5	28	48.3	10	2 A26381	hypertrehalosemic
6	26	44.8	8	2 S55310	adipokinetic hormo
7	26	44.8	8	2 A58620	adipokinetic hormo
8	26	44.8	9	2 PT0231	Ig heavy chain CDR
9	26	44.8	10	2 A46030	gonadoliberin I -
10	25	43.1	8	2 S15422	adipokinetic hormo
11	25	43.1	8	2 A33995	adipokinetic hormo
12	25	43.1	8	2 A58641	adipokinetic hormo
13	25	43.1	8	2 S21663	neuropeptide - flo
14	25	43.1	10	1 RHAQ2	gonadoliberin II -
15	25	43.1	10	1 A61126	gonadoliberin - sp
16	25	43.1	10	2 B46030	gonadoliberin II -
17	25	43.1	10	2 B33995	hypotrehalosemic h
18	25	43.1	10	2 A21114	gonadoliberin - ch
19	25	43.1	14	2 S33802	chaperone, TCP1-re
20	24	41.4	10	2 S39030	lysyl-bradykinin -
21	24	41.4	11	2 S70338	napin small chain
22	24	41.4	14	2 PH1322	Ig heavy chain DJ
23	23	39.7	9	2 PT0288	Ig heavy chain CRD
24	23	39.7	10	2 S65388	cytochrome-c oxida
25	23	39.7	10	2 S77990	cytochrome-c oxida
26	23	39.7	10	2 PT0289	Ig heavy chain CRD
27	23	39.7	11	2 S05002	corazonin - Americ
28	23	39.7	11	2 PT0302	Ig heavy chain CRD
29	22	37.9	8	2 S08995	hypertrehalosemic

30	22	37.9	8	2 A49823	adipokinetic hormo
31	22	37.9	8	2 A44960	neuropeptide led-C
32	22	37.9	8	2 A43976	hypertrehalosemic
33	22	37.9	8	2 B43976	hypertrehalosemic
34	22	37.9	8	2 A05169	neuropeptide M-I -
35	22	37.9	10	2 S53789	neuropeptide Pec-H
36	22	37.9	13	2 A60409	bombesin-like pept
37	22	37.9	13	2 S23640	Ig kappa chain J s
38	21	36.2	10	1 RHLMS	gonadoliberin - se
39	21	36.2	11	2 S68649	spermadhesin AQN-3
40	21	36.2	11	2 PT0209	T-cell receptor al
41	21	36.2	12	2 PT0274	Ig heavy chain CRD
42	21	36.2	14	2 S03530	Ig heavy chain J r
43	20	34.5	8	2 A28004	adipokinetic hormo
44	20	34.5	8	2 S10596	adipokinetic hormo
45	20	34.5	8	2 S11545	adipokinetic hormo

ALIGNMENTS

RESULT 1

A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61348; S07139
R;Fennlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A;Reference number: A61348; MUID:72228738; PMID:5041363
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
R;Fennlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis.
A;Reference number: S07139; MUID:75054965; PMID:4433569
A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E', 2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 2

A60421
hypertrehalosemic hormone - German cockroach
N;Alternate names: Bld-HrTH
C;Species: Blattella germanica (German cockroach)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C;Accession: A60421; S09137
R;Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella
A;Reference number: A60421; MUID:91179584; PMID:2080017
A;Accession: A60421
A;Molecule type: protein
A;Residues: 1-10 <VEE>

R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137

A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 3
S08997

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08997
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997

A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 4
S08998

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08998
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998

A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 5

A26381
hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: A26381
R;Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpus cardiacum of the cockroach Nauphoeta cinerea
A;Reference number: A26381; MUID:87100208; PMID:3801028
A;Accession: A26381

A;Molecule type: protein
A;Residues: 1-10 <GAD>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 6

S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N;Alternate names: Psi-AKH
C;Species: Pseudagrion inconspicuum
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: S55310
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum and Zygoptera
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: S55310

A;Molecule type: protein
A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: |||
Db 3 NFSPGW 8

RESULT 7

A58620
adipokinetic hormone - damselfly (Ischnura senegalensis)
C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum and Zygoptera
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: A58620

A;Molecule type: protein

A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVGPGW 6
: : |||
Db 3 NYTPGW 8

RESULT 8
PT0231
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0231
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0231
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 44.8%; Score 26; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
: : |||
Db 3 HSSGWVS 9

RESULT 9
A46030
gonadoliberin I - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Dec-1998
C;Accession: A46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: A46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HVGPGWV 7
: : |||
Db 2 HWSHGWL 8

RESULT 10
S15422
adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422

R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pig
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: S15422
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HVGPGW 6
: : |||
Db 3 NYSPDW 8

RESULT 11
A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: A33995
A;Molecule type: protein
A;Residues: 1-8 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 43.1%; Score 25; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
: : |||
Db 4 FTPGW 8

RESULT 12
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pig
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: A58641
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HVGPGW 6
: : |||
Db 3 NYSPDW 8

RESULT 13
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of various insects.
A;Reference number: S21663; MUID:92265187; PMID:1586453
A;Accession: S21663
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>

Query Match 43.1%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db 3 NYSPDW 8

RESULT 14
RHAQ2
gonadoliberin II - American alligator
N;Alternate names: gonadotropin-releasing hormone II
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: B60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson, Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of alligators.
A;Reference number: A60066; MUID:91352338; PMID:1882082
A;Accession: B60066
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db 2 HWSHGW 7

RESULT 15
A61126
gonadoliberin - spotted ratfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Hydrolagus colliei (spotted ratfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 18-Mar-1997
C;Accession: A61126
R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
Gen. Comp. Endocrinol. 82, 152-161, 1991
A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocarpine fish.
A;Reference number: A61126; MUID:91340067; PMID:1678723
A;Accession: A61126
A;Molecule type: protein
A;Residues: 1-10 <LOV>
A;Experimental source: brain
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db 2 HWSHGW 7

RESULT 16
B46030
gonadoliberin II - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jan-2003
C;Accession: B46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain protein.
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: B46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db 2 HWSHGW 7

RESULT 17
B33995
hypotrehalosemic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: B33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities.
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
Db 4 FTPGW 8

RESULT 18
A21114
gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.

Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing hormone.
A;Reference number: A21114; MUID:83195140; PMID:6341999
A;Accession: A21114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7
|: ||:
Db 2 HWSYGWL 8

RESULT 19

S33802
chaperone, TCPI-related - oat
C;Species: Avena sativa (oat)
C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C;Accession: S33802
R;Mumert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer
Nature 363, 644-648, 1993
A;Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo
A;Reference number: S33800; MUID:93288140; PMID:8099715
A;Accession: S33802
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <MUM>

Query Match 43.1%; Score 25; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWV 7
|: ||:
Db 8 GPWWI 12

RESULT 20

S39030
lysyl-bradykinin - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 18-Aug-2000
C;Accession: S39030
R;Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla
A;Reference number: S39030; MUID:94039817; PMID:8224232
A;Accession: S39030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <CON>
C;Superfamily: unassigned animal peptides

Query Match 41.4%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|: ||:
Db 4 PGW 6

RESULT 21

S70338
napin small chain S3A - Swedish turnip (fragment)
C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70338
R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.

Biochim. Biophys. Acta 1295, 23-33, 1996
A;Title: Purification and sequencing of multiple forms of Brassica napus seed napin small
A;Reference number: S70336; MUID:96283790; PMID:8679670
A;Accession: S70338
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NEU>

Query Match 41.4%; Score 24; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
|: ||:
Db 8 GPSW 11

RESULT 22

PH1322
Ig heavy chain DJ region (clone C344-99) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1322
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1322
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 41.4%; Score 24; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
|: ||:
Db 2 WSGGW 6

RESULT 23

PT0288
Ig heavy chain CRD3 region (clone 4-106) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0288
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jo
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0288
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6
|: ||:
Db 5 YSSGW 9

RESULT 24

S65388
cytochrome-c oxidase (BC 1.9.3.1) chain VII c, hepatic - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S65388; S65389
R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65388
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SCH>
A;Accession: S65389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SC2>
C;Superfamily: cytochrome-c oxidase chain VIIC
C;Keywords: oxidoreductase

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 HY--GPG 5
| | | | |
Db 2 HYEAGPG 8

RESULT 25
S77990
cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77990
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77990
A;Molecule type: protein
A;Residues: 1-10 <ARN>
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 HY--GPG 5
| | | | |
Db 2 HYEAGPG 8

RESULT 26
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 WVSM 9
| : | |

Db 4 WISM 7

RESULT 27

S05002
corazonin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998
C;Accession: S05002
R;Veenstra, J.A.
FEBS Lett. 250, 231-234, 1989
A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american
A;Reference number: S05002; MUID:89325572; PMID:2753132
A;Accession: S05002
A;Molecule type: protein
A;Residues: 1-11 <VEE>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 39.7%; Score 23; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGPGWVS 8

| | | |

Db 5 YSRGWTN 11

RESULT 28

PT0302
Ig heavy chain CRD3 region (clone 5-112) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0302
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0302
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6

| | | |

Db 6 YSSGW 10

RESULT 29

S08995
hypertrehalosemic hormone I - oriental cockroach
N;Alternate names: Pea-CAH-I
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S08995
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08995
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 30

A49823
adipokinetic hormone I - American cockroach
N;Alternate names: periplanetin CC-1
C;Species: Periplaneta americana (American cockroach)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: A49823
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
A;Reference number: A49823; MUID:84298179; PMID:6591205
A;Accession: A49823
A;Molecule type: protein
A;Residues: 1-8 <SCA>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 31

A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 32

A43976
hypertrehalosemic hormone - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: A43976
R;Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990

A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid bee
A;Reference number: A43976; MUID:90341081; PMID:2381871
A;Accession: A43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 33

B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C;Accession: B43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid bee
A;Reference number: A43976; MUID:90341081; PMID:2381871
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 34

A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass
A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 35

S53789

neuropeptide Pec-HrTH - Platypleura capensis
C;Species: Platypleura capensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S53789
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose
A;Reference number: S53789; MUID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 37.9%; Score 22; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.2e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
: : | |
Db 3 NFSPSW 8

RESULT 36
A60409
bombesin-like peptide L - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C;Accession: A60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: A60409
A;Molecule type: protein
A;Residues: 1-13 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;13/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
| | |
Db 4 GPQW 7

RESULT 37
S23640
Ig kappa chain J segment (J-kappa-3) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S23640
R;Huber, C.; Klobeck, H.G.; Zachau, H.G.
Eur. J. Immunol. 22, 1561-1565, 1992
A;Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa
A;Reference number: S23637; MUID:92289816; PMID:1601042
A;Accession: S23640
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <HUB>
A;Cross-references: EMBL:X63370
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
C;Keywords: heterotetramer; immunoglobulin

Query Match 37.9%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGPG 5
: | | |

Db 3 FGPG 6

RESULT 38
RHLMGS
gonadoliberin - sea lamprey
N;Alternate names: gonadotropin releasing hormone (GnRH)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
C;Accession: A01412
R;Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J. Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; MUID:86168192; PMID:3514603
A;Accession: A01412
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Comment: This hormone was isolated from the brain.
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.2%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYGPGW 6
| | |
Db 2 HYSLEW 7

RESULT 39
S68649
spermadhesin AQN-3 - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
C;Accession: S68649
R;Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adermann, K.; Thole, H.H.; Toepfer-Petersen, E
FEBS Lett. 379, 207-211, 1996
A;Title: Mapping the heparin-binding domain of boar spermadhesins.
A;Reference number: S68648; MUID:96184566; PMID:8603690
A;Accession: S68649
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6;7-11 <CAL>

Query Match 36.2%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GWV 7
| | |
Db 5 GWV 7

RESULT 40
PT0209
T-cell receptor alpha chain V-J region (4-1-L.6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0209
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0209
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 36.2%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYG 3
|||
Db 6 HYG 8

RESULT 41
PT0274
Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0274
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0274
A;Molecule type: DNA
A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 36.2%; Score 21; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
| | |
Db 3 YSSSWTS 9

RESULT 42
S03530
Ig heavy chain J region (JH-4) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
C;Accession: S03530
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop
A;Reference number: S01158; MUID:89052653; PMID:2903824
A;Accession: S03530
A;Molecule type: DNA
A;Residues: 1-14 <SCH>
A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33043.1; PID:gl334657

Query Match 36.2%; Score 21; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPG 5
| : |
Db 3 HWGQG 7

RESULT 43
A28004
adipokinetic hormone G - two-spotted cricket
N;Alternate names: AKH-G
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C;Accession: A28004
R;Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pepti
A;Reference number: A28004; MUID:88106553; PMID:3426616
A;Accession: A28004
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.5%; Score 20; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
: : |
Db 3 NFSTGW 8

RESULT 44

S10596

adipokinetic hormone - pond skimmer

C;Species: Libellula auripennis

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C;Accession: S10596

R;Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor

A;Reference number: S10596; MUID:90359055; PMID:2390213

A;Accession: S10596

A;Molecule type: protein

A;Residues: 1-8 <BIO>

C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.5%; Score 20; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
: : |
Db 3 NPTPSW 8

RESULT 45

S11545

adipokinetic hormone - nestling-sucking blowfly

C;Species: Protophormia terraenovae (nestling-sucking blowfly)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997

C;Accession: S11545

R;Gaede, G.; Wilps, H.; Kellner, R.

Biochem. J. 269, 309-313, 1990

A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

erraenovae (Diptera).

A;Reference number: S11545; MUID:90351345; PMID:2386478

A;Accession: S11545

A;Molecule type: protein

A;Residues: 1-8 <GAE>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.5%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6
: |
Db 4 FSPDW 8

Search completed: August 30, 2004, 10:58:52
Job time : 3.70608 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58	100.0	14	15	US-10-394-980-52	Sequence 52, Appli
2	31	53.4	8	10	US-09-849-092-2	Sequence 2, Appli
3	31	53.4	11	11	US-09-791-551-99	Sequence 99, Appli
4	30	51.7	8	10	US-09-880-748-2870	Sequence 2870, Ap
5	30	51.7	8	12	US-10-293-418-2870	Sequence 2870, Ap
6	28	48.3	8	15	US-10-186-229-90	Sequence 90, Appli
7	28	48.3	10	14	US-10-072-419-2	Sequence 2, Appli
8	28	48.3	11	12	US-10-417-895A-53	Sequence 53, Appli
9	28	48.3	13	16	US-10-468-370-599	Sequence 599, App
10	27.5	47.4	13	16	US-10-381-112-51	Sequence 51, Appli
11	27.5	47.4	13	16	US-10-381-112-91	Sequence 91, Appli
12	27.5	47.4	14	16	US-10-381-112-31	Sequence 31, Appli
13	27.5	47.4	14	16	US-10-381-112-50	Sequence 50, Appli
14	27.5	47.4	14	16	US-10-381-112-82	Sequence 82, Appli
15	27	46.6	10	14	US-10-190-082-450	Sequence 450, App

16	27	46.6	11	9	US-09-861-597-12	Sequence 12, Appl
17	27	46.6	12	14	US-10-286-457-411	Sequence 411, App
18	26.5	45.7	8	10	US-09-863-600E-28	Sequence 28, Appl
19	26.5	45.7	11	10	US-09-863-600E-17	Sequence 17, Appl
20	26.5	45.7	11	12	US-10-609-217-429	Sequence 429, App
21	26.5	45.7	11	12	US-10-609-217-1040	Sequence 1040, Ap
22	26.5	45.7	11	12	US-10-632-388-429	Sequence 429, App
23	26.5	45.7	11	12	US-10-632-388-1040	Sequence 1040, Ap
24	26.5	45.7	11	12	US-10-651-723-429	Sequence 429, App
25	26.5	45.7	11	12	US-10-651-723-1040	Sequence 1040, Ap
26	26.5	45.7	11	12	US-10-645-761-429	Sequence 429, App
27	26.5	45.7	11	12	US-10-645-761-1040	Sequence 1040, Ap
28	26.5	45.7	11	16	US-10-666-696-429	Sequence 429, App
29	26.5	45.7	11	16	US-10-666-696-1040	Sequence 1040, Ap
30	26.5	45.7	11	16	US-10-653-048-429	Sequence 429, App
31	26.5	45.7	11	16	US-10-653-048-1040	Sequence 1040, Ap
32	26.5	45.7	12	10	US-09-863-600E-18	Sequence 18, Appl
33	26.5	45.7	12	10	US-09-863-600E-25	Sequence 25, Appl
34	26.5	45.7	12	12	US-10-609-217-1041	Sequence 1041, Ap
35	26.5	45.7	12	12	US-10-632-388-1041	Sequence 1041, Ap
36	26.5	45.7	12	12	US-10-651-723-1041	Sequence 1041, Ap
37	26.5	45.7	12	12	US-10-645-761-1041	Sequence 1041, Ap
38	26.5	45.7	12	14	US-10-271-343-14	Sequence 14, Appl
39	26.5	45.7	12	16	US-10-666-696-1041	Sequence 1041, Ap
40	26.5	45.7	12	16	US-10-653-048-1041	Sequence 1041, Ap
41	26.5	45.7	13	10	US-09-863-600E-16	Sequence 16, Appl
42	26.5	45.7	13	12	US-10-609-217-428	Sequence 428, App
43	26.5	45.7	13	12	US-10-609-217-1039	Sequence 1039, Ap
44	26.5	45.7	13	12	US-10-632-388-428	Sequence 428, App
45	26.5	45.7	13	12	US-10-632-388-1039	Sequence 1039, Ap

ALIGNMENTS

RESULT 1
US-10-394-980-52
; Sequence 52, Application US/10394980
; Publication No. US20040005633A1
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: part of CYPB_HUMAN (peptidyl-prolyl cis-trans isomerase B)
US-10-394-980-52

Query Match 100.0%; Score 58; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HYGPGWVSM 9
Db 1 HYGPGWVSM 9


```
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2870
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2870
```

```
Query Match      51.7%; Score 30; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GPGW 6
      ||||
Db      2 GPGW 5
```

```
RESULT 6
US-10-186-229-90
; Sequence 90, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; FILE REFERENCE: 11669.108US01
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-90
```

```
Query Match      48.3%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 PGWV 7
      ||||
Db      4 PGWV 7
```

```
RESULT 7
US-10-072-419-2
; Sequence 2, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Gromphadorhina portentosa
US-10-072-419-2
```

```
Query Match      48.3%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HYGPW 6
      :: |||
Db      3 NFSPW 8
```

```
RESULT 8
US-10-417-895A-53
; Sequence 53, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-53
```

```
Query Match      48.3%; Score 28; DB 12; Length 11;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 HYGPWVS 8
      :|||
Db      2 YGSSWYS 9
```

```
RESULT 9
US-10-468-370-599
; Sequence 599, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599
```

```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-599

Query Match      48.3%; Score 28; DB 16; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GPGWV 7
      |||||
Db      8 GPNWV 12

RESULT 10
US-10-381-112-51
; Sequence 51, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 51
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 13
; OTHER INFORMATION: C-terminal amidation
US-10-381-112-51

Query Match      47.4%; Score 27.5; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      3 GP-GWVSM 9
      |||||
Db      6 GPWGWVCM 13

RESULT 11
US-10-381-112-91
; Sequence 91, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
```

```
; SEQ ID NO 91
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGE receptor binding peptide described in Example 6
US-10-381-112-91

Query Match      47.4%; Score 27.5; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      3 GP-GWVSM 9
      |||||
Db      6 GPWGWVCM 13

RESULT 12
US-10-381-112-31
; Sequence 31, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: clone g3c.21 shown in Table 4
US-10-381-112-31

Query Match      47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      3 GP-GWVSM 9
      |||||
Db      4 GPWGWVCM 11

RESULT 13
US-10-381-112-50
; Sequence 50, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 50
; LENGTH: 14
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IgE receptor binding peptide of Table 5. IgE068
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 14
; OTHER INFORMATION: C-terminal amidation
US-10-381-112-50
```

```
Query Match          47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      3 GP-GWVSM 9
      || |||||
Db       7 GPWGWVCM 14
```

```
RESULT 14
US-10-381-112-82
; Sequence 82, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovashnik, Melissa A.
; TITLE OF INVENTION: IgE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; PRIOR FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 82
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IgE receptor binding peptide of Table 5. IgE107
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: N-terminal acetylation
US-10-381-112-82
```

```
Query Match          47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      3 GP-GWVSM 9
      || |||||
Db       7 GPWGWVCM 14
```

```
RESULT 15
US-10-190-082-450
; Sequence 450, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 450
```

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-450
```

```
Query Match          46.6%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 PGWVSM 9
      |||||
Db       3 PGWWSL 8
```

```
RESULT 16
US-09-861-597-12
; Sequence 12, Application US/09861597
; Patent No. US20020064539A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPPE, Michel
; APPLICANT: GARSON, Jean-Claude
; APPLICANT: ARRAUDEAU, Jean-Pierre
; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; TITLE OF INVENTION: ANALOG
; FILE REFERENCE: 6388-0365-0
; CURRENT APPLICATION NUMBER: US/09/861,597
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/247,806
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: FR 98/01614
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa corresponds to the amino acid sequence GPS or
; OTHER INFORMATION: GPG
; OTHER INFORMATION: Description of Artificial Sequence:protein
US-09-861-597-12
```

```
Query Match          46.6%; Score 27; DB 9; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 YGPGWVS 8
      |||||
Db       4 YGPGQXS 10
```

```
RESULT 17
US-10-286-457-411
; Sequence 411, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 411
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

;
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-411

Query Match 46.6%; Score 27; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HYGPGWVS 8
| | | |
Db 3 HQASGWTS 10

RESULT 18
US-09-863-600E-28
; Sequence 28, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-28

Query Match 45.7%; Score 26.5; DB 10; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
| | | |
Db 1 HFGPLTWV 8

RESULT 19
US-09-863-600E-17
; Sequence 17, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-17

Query Match 45.7%; Score 26.5; DB 10; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
| | | |
Db 3 HFGPLTWV 10

RESULT 20
US-10-609-217-429
; Sequence 429, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
| | | |
Db 3 HFGPLTWV 10

RESULT 21
US-10-609-217-1040
; Sequence 1040, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 22

US-10-632-388-429
; Sequence 429, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 23

US-10-632-388-1040
; Sequence 1040, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE

US-10-632-388-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 24

US-10-651-723-429
; Sequence 429, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 25

US-10-651-723-1040
; Sequence 1040, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 26
US-10-645-761-429
; Sequence 429, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 27
US-10-645-761-1040
; Sequence 1040, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 28
US-10-666-696-429
; Sequence 429, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-429

Query Match 45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 29
US-10-666-696-1040
; Sequence 1040, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
US-10-666-696-1040

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO MIMETIC PEPTIDE
US-10-666-696-1040

Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|
Db      3 HFGPLTWV 10

RESULT 30
US-10-653-048-429
; Sequence 429, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-429

Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|
Db      3 HFGPLTWV 10

RESULT 31
US-10-653-048-1040
; Sequence 1040, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1040
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```
Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
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```
QY      1 HYGP-GWV 7
      |:|:|
Db      3 HFGPLTWV 10
```

```
RESULT 32
US-09-863-600E-18
; Sequence 18, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-18
```

```
Query Match      45.7%; Score 26.5; DB 10; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 HYGP-GWV 7
      |:|:|
Db      3 HFGPLTWV 10
```

```
RESULT 33
US-09-863-600E-25
; Sequence 25, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-25

Query Match          45.7%; Score 26.5; DB 10; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:|
Db 4 HFGPLTWV 11

RESULT 34
US-10-609-217-1041
; Sequence 1041, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1041

Query Match          45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:|
Db 3 HFGPLTWV 10

RESULT 35
US-10-632-388-1041
; Sequence 1041, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-1041
```

```
US-10-632-388-1041

Query Match          45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:|
Db 3 HFGPLTWV 10

RESULT 36
US-10-651-723-1041
; Sequence 1041, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-1041

Query Match          45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:|
Db 3 HFGPLTWV 10

RESULT 37
US-10-645-761-1041
; Sequence 1041, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-1041
```

```
Query Match      45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:| ||
Db 3 HFGPLTWV 10

RESULT 38
US-10-271-343-14
; Sequence 14, Application US/10271343
; Publication No. US20030166003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
US-10-271-343-14

Query Match      45.7%; Score 26.5; DB 14; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:| ||
Db 3 HFGPLTWV 10

RESULT 39
US-10-666-696-1041
; Sequence 1041, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
```

```
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-1041

Query Match      45.7%; Score 26.5; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:| ||
Db 3 HFGPLTWV 10

RESULT 40
US-10-653-048-1041
; Sequence 1041, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1041

Query Match      45.7%; Score 26.5; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
   |:|:| ||
Db 3 HFGPLTWV 10

RESULT 41
US-09-863-600E-16
; Sequence 16, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
```

US-09-863-600E-16

Query Match 45.7%; Score 26.5; DB 10; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 42

US-10-609-217-428
; Sequence 428, Application US/10609217
; Publication No. US2004004188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-428

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 43

US-10-609-217-1039
; Sequence 1039, Application US/10609217
; Publication No. US2004004188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1039
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1039

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 44

US-10-632-388-428
; Sequence 428, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-428

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 45

US-10-632-388-1039
; Sequence 1039, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1039
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-1039

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HVGPGWV 7
Db 4 HFGPLTWV 11

Search completed: August 30, 2004, 11:05:00
Job time : 12.0068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	34	58.6	14	5	PCT-US93-06751-120
2	32	55.2	8	1	US-08-271-830-56
3	31	53.4	8	1	US-08-375-962B-2
4	31	53.4	8	2	US-08-562-114B-2
5	31	53.4	8	3	US-08-729-594A-2
6	31	53.4	8	4	US-08-937-993-2
7	30	51.7	13	5	PCT-US93-06751-66
8	30	51.7	14	5	PCT-US93-06751-93
9	29	50.0	11	6	5164481-10
10	29	50.0	14	5	PCT-US93-06751-65
11	28	48.3	10	1	US-08-353-400-26
12	28	48.3	10	2	US-08-747-137-122
13	28	48.3	11	2	US-08-598-873-68
14	28	48.3	11	3	US-08-605-430-68
15	28	48.3	12	2	US-08-406-330-33
16	28	48.3	12	2	US-08-556-597-33
17	28	48.3	14	5	PCT-US93-06751-67
18	28	48.3	14	5	PCT-US93-06751-103
19	27	46.6	11	2	US-08-665-202-97
20	27	46.6	11	2	US-08-665-202-105
21	27	46.6	11	3	US-09-247-806-12
22	27	46.6	11	4	US-09-315-574-97
23	27	46.6	11	4	US-09-315-574-105
24	27	46.6	13	5	PCT-US93-06751-102
25	27	46.6	14	5	PCT-US93-06751-63
26	26.5	45.7	8	1	US-08-484-635-201
27	26.5	45.7	8	2	US-08-484-631-201

28	26.5	45.7	8	2	US-08-827-570-201	Sequence 201, App
29	26.5	45.7	11	1	US-08-484-135-17	Sequence 17, Appl
30	26.5	45.7	11	1	US-08-484-635-17	Sequence 17, Appl
31	26.5	45.7	11	2	US-08-484-631-17	Sequence 17, Appl
32	26.5	45.7	11	2	US-08-827-570-17	Sequence 17, Appl
33	26.5	45.7	11	3	US-08-905-310-11	Sequence 11, Appl
34	26.5	45.7	11	4	US-09-428-082B-429	Sequence 429, App
35	26.5	45.7	11	4	US-09-428-082B-1040	Sequence 1040, Ap
36	26.5	45.7	12	1	US-08-484-135-18	Sequence 18, Appl
37	26.5	45.7	12	1	US-08-484-635-200	Sequence 200, App
38	26.5	45.7	12	1	US-08-484-635-246	Sequence 246, App
39	26.5	45.7	12	1	US-08-484-631-200	Sequence 200, App
40	26.5	45.7	12	2	US-08-484-631-246	Sequence 246, App
41	26.5	45.7	12	2	US-08-827-570-200	Sequence 200, App
42	26.5	45.7	12	2	US-08-827-570-246	Sequence 246, App
43	26.5	45.7	12	3	US-08-786-690-3	Sequence 3, Appli
44	26.5	45.7	12	4	US-09-428-082B-1041	Sequence 1041, Ap
45	26.5	45.7	13	1	US-08-484-135-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
PCT-US93-06751-120
; Sequence 120, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Beta
PCT-US93-06751-120

Query Match 58.6%; Score 34; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYPGW 5
|||||

Db 7 HYPGW 11

RESULT 2

US-08-271-830-56
; Sequence 56, Application US/08271830
; Patent No. 5510332
; GENERAL INFORMATION:
; APPLICANT: Kogan, Timothy P.
; APPLICANT: Ren, Kaijun
; APPLICANT: Vanderslice, Peter
; APPLICANT: Beck, Pamela J.
; TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
; TITLE OF INVENTION: INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
; TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 5510332th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,830
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5510332thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /label= xaa
; OTHER INFORMATION: /note= "Xaa=Pro-NH2."
US-08-271-830-56

Query Match 55.2%; Score 32; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWVSM 9

Db 1 GPGWLDV 7

RESULT 3

US-08-375-962B-2
; Sequence 2, Application US/08375962B
; Patent No. 5731195
; GENERAL INFORMATION:
; APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
; APPLICANT: CRISTER, ERIKSSON, ULF.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecule
; TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
; TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
; TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-962B-2

Query Match 53.4%; Score 31; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6

Db 1 YSPGW 5

RESULT 4

US-08-562-114B-2
; Sequence 2, Application US/08562114B
; Patent No. 5972646
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON ET AL.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A
; TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
; TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect 5.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/562,114B
; FILING DATE: 22-No. 5972646ember-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohli, Vineet

; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-562-114B-2

Query Match 53.4%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
| | | |
Db 1 YSPGW 5

RESULT 5
US-08-729-594A-2
; Sequence 2, Application US/08729594A
; Patent No. 6280997
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,594A
; FILING DATE: 11-October-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/562,114
; FILING DATE: 22-No. 6280997ember-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; APPLICATION DATA:
; FILING DATE: 10-June-1994
; NAME: Hanson, No. 6280997man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5372.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-594A-2

Query Match 53.4%; Score 31; DB 3; Length 8;

Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
| | | |
Db 1 YSPGW 5

RESULT 6
US-08-937-993-2
; Sequence 2, Application US/08937993
; Patent No. 6399344
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
; TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
; TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,993
; FILING DATE: September 26, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/729,594
; FILING DATE: 11-October-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/562,114
; FILING DATE: 22-No. 6399344ember-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; APPLICATION DATA:
; FILING DATE: 10-June-1994
; NAME: Hanson, No. 6399344man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-993-2

Query Match 53.4%; Score 31; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
| | | |
Db 1 YSPGW 5

RESULT 7
PCT-US93-06751-66
; Sequence 66, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold

```

; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
; PCT-US93-06751-66

Query Match 51.7%; Score 30; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
Db 4 HFGPG 8

RESULT 8
PCT-US93-06751-93
; Sequence 93, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Gamma
; PCT-US93-06751-93

Query Match 51.7%; Score 30; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
Db 4 HFGPG 8

RESULT 9
5164481-10
; Patent No. 5164481
; APPLICANT: LACROIX, MARTIAL;ZREIN, MAAN;DIONNE, GERVAIS
; TITLE OF INVENTION: PEPTIDES AND ANALOGUES AND MIXTURES
; FOR DETECTING AND ELICITING ANTIBODIES TO RUBELLA VIRUS
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/397,767
; FILING DATE: 23-AUG-1989
; SEQ ID NO:10:
; LENGTH: 11
5164481-10

Query Match 50.0%; Score 29; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
Db 2 HGPDWAS 8

RESULT 10
PCT-US93-06751-65
; Sequence 65, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

/ FILING DATE: 19930719
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meredith, Roy D.
/ REGISTRATION NUMBER: 30,777
/ REFERENCE/DOCKET NUMBER: 18614
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 594-4678
/ TELEFAX: (908) 594-4720
/ TELEX: 138825
/ INFORMATION FOR SEQ ID NO: 65:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-65

Query Match 50.0%; Score 29; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
|:|
Db 4 HWGPG 8

RESULT 11
US-08-353-400-26
/ Sequence 26, Application US/08353400
/ Patent No. 5665357
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 37
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/353,400
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9324819.3
/ FILING DATE: 03-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9411089.7
/ FILING DATE: 03-JUN-1994
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-353-400-26

Query Match 48.3%; Score 28; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
|:|
Db 4 HRGSGW 9

RESULT 12

US-08-747-137-122
/ Sequence 122, Application US/08747137
/ Patent No. 5945033
/ GENERAL INFORMATION:
/ APPLICANT: YEN, Richard C.K.
/ TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
/ TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
/ NUMBER OF SEQUENCES: 184
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/747,137
/ FILING DATE: 12-NOV-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/212,546
/ FILING DATE: 14-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/069,831
/ FILING DATE: 01-JUN-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/959,560
/ FILING DATE: 13-OCT-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/641,720
/ FILING DATE: 15-JAN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 016197-000840US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-576-0200
/ INFORMATION FOR SEQ ID NO: 122:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /product= "p-Glu"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 10
/ OTHER INFORMATION: /product= "Thr-Amide"
US-08-747-137-122

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
|:|
Db 3 NFSPGW 8

RESULT 13
US-08-598-873-68
/ Sequence 68, Application US/08598873
/ Patent No. 5928884
/ GENERAL INFORMATION:
/ APPLICANT: Croce, Carlo M.


```

; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: FHIT PROTEINS AND NUCLEIC ACIDS AND
; METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebel, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-598-873-68

Query Match      48.3%; Score 28; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYPG 4
      ||||
Db      1 HYPG 4

RESULT 14
US-08-605-430-68
; Sequence 68, Application US/08605430
; Patent No. 6242212
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; ADDRESSEE: Huebner, Kay
; TITLE OF INVENTION: FHIT PROTEINS AND NUCLEIC ACIDS AND
; METHODS BASED THEREON
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,430
; FILING DATE: 22-FEB-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebel, Thomas E.

```

```

; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-605-430-68

Query Match      48.3%; Score 28; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYPG 4
      ||||
Db      1 HYPG 4

RESULT 15
US-08-406-330-33
; Sequence 33, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-33

Query Match      48.3%; Score 28; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YGPGWV 7
      :|||
Db      3 FGPFVW 8

```

RESULT 16
US-08-556-597-33
; Sequence 33, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-556-597-33

Query Match 48.3%; Score 28; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGPGWV 7
:| | | |
Db 3 FGPFVW 8

RESULT 17
PCT-US93-06751-67
; Sequence 67, Application PC/TUS93306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Gamma
; PCT-US93-06751-67

Query Match 48.3%; Score 28; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGP 4
:| | | |
Db 4 HYGP 7

RESULT 18
PCT-US93-06751-103
; Sequence 103, Application PC/TUS93306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-103

Query Match 48.3%; Score 28; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
:||||
Db 4 YGPG 8

RESULT 19

US-08-665-202-97
; Sequence 97, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-97

Query Match 46.6%; Score 27; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPGWV 7
:| |||
Db 5 YYRSGWV 11

RESULT 20

US-08-665-202-105
; Sequence 105, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-105

Query Match 46.6%; Score 27; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPGWV 7
:| |||
Db 5 YYRSGWV 11

RESULT 21

US-09-247-806-12
; Sequence 12, Application US/09247806
; Patent No. 6280747
; GENERAL INFORMATION:
; APPLICANT: PHILLIPPE, Michel
; APPLICANT: GARSON, Jean-Claude
; APPLICANT: ARRAUDEAU, Jean-Pierre
; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
; LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; ANALOG
; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; FILE REFERENCE: 6388-0365-0
; CURRENT APPLICATION NUMBER: US/09/247,806
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: FR 98/01614
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa corresponds to the amino acid sequence GPS or
; OTHER INFORMATION: GPG
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:protein
US-09-247-806-12

Query Match 46.6%; Score 27; DB 3; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
|||
Db 4 YGPGQXS 10

RESULT 22
US-09-315-574-97
; Sequence 97, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-97

Query Match 46.6%; Score 27; DB 4; Length 11;

Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HYGPGWV 7
:|
Db 5 YYRSGWV 11

RESULT 23
US-09-315-574-105
; Sequence 105, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; FILING DATE: 13-JUN-1996
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-105

Query Match 46.6%; Score 27; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7
:|
Db 5 YYRSGWV 11

RESULT 24
PCT-US93-06751-102
; Sequence 102, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold

```
;
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
; PCT-US93-06751-102

Query Match 46.6%; Score 27; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
Db 4 NYGPG 8

RESULT 25
PCT-US93-06751-63
; Sequence 63, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
; PCT-US93-06751-63

Query Match 46.6%; Score 27; DB 5; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPGWV 7
Db 4 HLGPGRV 10

RESULT 26
US-08-484-635-201
; Sequence 201, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-201

Query Match 45.7%; Score 26.5; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
|:|:|
Db 1 HFGPLTWV 8

RESULT 27
US-08-484-631-201
; Sequence 201, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-201

Query Match 45.7%; Score 26.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
|:|:|
Db 1 HFGPLTWV 8

RESULT 28
US-08-827-570-201
; Sequence 201, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-201

Query Match 45.7%; Score 26.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
|:|:|
Db 1 HFGPLTWV 8

RESULT 29
US-08-484-135-17
; Sequence 17, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza

; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A..
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-17

Query Match 45.7%; Score 26.5; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:| | |
Db 3 HFGPLTWV 10

RESULT 30
US-08-484-635-17
; Sequence 17, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:

; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-17

Query Match 45.7%; Score 26.5; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:| | |
Db 3 HFGPLTWV 10

RESULT 31
US-08-484-631-17
; Sequence 17, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-17


```
Query Match      45.7%; Score 26.5; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
```

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 32
US-08-827-570-17
; Sequence 17, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:

Query Match	45.7%	Score 26.5;	DB 2;	Length 11;
Best Local Similarity	62.5%;	Pred. No. 2.8e+02;		
Matches	5; Conservative	1; Mismatches	1; Indels	1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:|
pb 3 HEGPI.TWV 10

RESULT 33
US-08-905-310-11

```

; Sequence 11, Application US/08905310
; Patent No. 6077939
; GENERAL INFORMATION:
; APPLICANT: Wei, Ziping
; APPLICANT: Menon-Rudolph, Sunitha
; APPLICANT: Ghosh-Dastidar, Pradip
; TITLE OF INVENTION: Polypeptides Having a Single Covalently Bound
; TITLE OF INVENTION: N-Terminal Water-Soluble Polymer, and Related Methods,
; TITLE OF INVENTION: Compositions and Kits
; FILE REFERENCE: SEQUENCE LISTING ORT 843
; CURRENT APPLICATION NUMBER: US/08/905,310
; CURRENT FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide fragment
; US-08-905-310-11

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Query Match	45.7%	Score 26.5;	DB 3;	Length 11;
Best Local Similarity	62.5%	Pred. No. 2.8e+02;		
Matches	5;	Conservative	1;	Mismatches 1;
				Indels 1;
				Gaps 1;

QY 1 HYGP-GWV 7
| : | | |
Db 3 HFGPLTWV 10

```

RESULT 34
US-09-428-082B-429
; Sequence 429, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-429

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Query Match	45.7%	Score 26.5;	DB 4;	Length 11;
Best Local Similarity	62.5%	Pred. No. 2.8e+02;		
Matches	5;	Conservative	1;	Mismatches 1;
				Indels 1;
				Gaps 1;

QY 1 HYGP-GWV 7
|:|:|:|
db 3 HFGPLTWV 10

RESULT 35
US-09-428-082B-1040
; Sequence 1040, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.

; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-1040

Query Match 45.7%; Score 26.5; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 36
US-08-484-135-18
; Sequence 18, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. Digiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A..
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-135-18

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |

Db 3 HFGPLTWV 10
RESULT 37
US-08-484-635-200
; Sequence 200, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-200

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 38
US-08-484-635-246
; Sequence 246, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana

```
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-246

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 4 HFGPLTWV 11

RESULT 39
US-08-484-631-200
; Sequence 200, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-246
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-200

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 40
US-08-484-631-246
; Sequence 246, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-200
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; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-246

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 41
US-08-827-570-200
; Sequence 200, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-200

Query Match 45.7%; Score 26.5; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 42
US-08-827-570-246
; Sequence 246, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-246

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 43
US-08-786-690-3
; Sequence 3, Application US/08786690
; Patent No. 6221608

GENERAL INFORMATION:
APPLICANT: Middleton, Steven
APPLICANT: Johnson, Dana
APPLICANT: McMahon, Frank
APPLICANT: Mulkahy, Linda
APPLICANT: Jolliffe, Linda
TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
TITLE OF INVENTION: ERYTHROPOIETIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,690
FILING DATE: 08 August 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-821
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-2806
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
US-08-786-690-3

Query Match 45.7%; Score 26.5; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 44
US-09-428-082B-1041
Sequence 1041, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1041
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-1041

Query Match 45.7%; Score 26.5; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 3 HFGPLTWV 10

RESULT 45
US-08-484-135-16
Sequence 16, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. DiGiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-16

Query Match 45.7%; Score 26.5; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:|
Db 4 HFGPLTWV 11

Search completed: August 30, 2004, 10:57:18
Job time : 4.55743 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s.*
2: Geneseqp1990s.*
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4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	58	100.0	9	3	AAY69928	Aay69928 Human cyc
2	58	100.0	14	6	ABP74769	Abp74769 Proteome
3	49	84.5	10	3	AAY69947	Aay69947 Human cyc
4	49	84.5	10	6	ABR84352	Abr84352 Human Cyp
5	45	77.6	11	3	AAY69925	Aay69925 Human cyc
6	34	58.6	14	2	AAR47787	Aar47787 HIV epito
7	32	55.2	8	2	AAR95759	Aar95759 Alpha-4Be
8	31	53.4	8	2	AAR88101	Aar88101 Bovine p3
9	31	53.4	8	2	AAR18339	Aaw18339 Bovine p3
10	31	53.4	8	2	AAY01990	Aay01990 Tryptic p
11	30	51.7	8	5	ABP46859	Abp46859 Human Bly
12	30	51.7	9	1	AAP95363	Aap95363 Variable
13	30	51.7	9	2	AAR31288	Aar31288 HIV princ
14	30	51.7	9	2	AAR30043	Aar30043 HIV princ
15	30	51.7	9	2	AAR26724	Aar26724 HIV-PND-p
16	30	51.7	11	5	AAY98826	Aau98826 Adenoviru
17	30	51.7	12	5	AAY83484	Aau83484 PPV V1up
18	30	51.7	13	2	AAR47733	Aar47733 HIV epito
19	30	51.7	14	2	AAR47760	Aar47760 HIV epito
20	29	50.0	10	7	ADD94624	Add94624 Human SIM
21	29	50.0	14	2	AAR47732	Aar47732 HIV epito
22	29	50.0	14	4	AAM98717	Aam98717 Human pep
23	28	48.3	8	4	ABB45010	Abb45010 Human alb
24	28	48.3	10	2	AAR76078	Aar76078 Phage dis
25	28	48.3	10	2	AAY31073	Aay31073 Non-cross

26	28	48.3	10	7	ADC07128	Adc07128 Giant Mad
27	28	48.3	12	2	AAW32655	Aaw32655 Human pla
28	28	48.3	12	2	AAW71785	Aaw71785 Mimotope
29	28	48.3	13	5	AAE27766	Aae27766 Human bet
30	28	48.3	14	2	AAR47734	Aar47734 HIV epito
31	28	48.3	14	2	AAR47770	Aar47770 HIV epito
32	28	48.3	14	3	AAY57711	Aay57711 Rat clust
33	27.5	47.4	13	5	ABG66144	Abg66144 IGE Fceps
34	27.5	47.4	13	5	ABG66104	Abg66104 IGE Fceps
35	27.5	47.4	14	5	ABG66135	Abg66135 IGE Fceps
36	27.5	47.4	14	5	ABG66084	Abg66084 IGE Fceps
37	27.5	47.4	14	5	ABG66103	Abg66103 IGE Fceps
38	27	46.6	8	6	AAE34589	Aae34589 Phage pep
39	27	46.6	9	4	AAB70713	Aab70713 Human TAA
40	27	46.6	10	2	AAR31271	Aar31271 HIV princ
41	27	46.6	10	2	AAR31308	Aar31308 Cyclic HI
42	27	46.6	10	2	AAR26707	Aar26707 HIV-PND-p
43	27	46.6	11	2	AAW08545	Aaw08545 C6 human
44	27	46.6	11	2	AAW08535	Aaw08535 C6 human
45	27	46.6	12	7	ADC44682	Adc44682 Endotheli

ALIGNMENTS

RESULT 1
AAY69928
ID AAY69928 standard; peptide; 9 AA.
XX
AC AAY69928;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #8.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
(SUMU) SUMITOMO PHARM CO LTD.
(ITOH/) ITOH K.
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYGPGWVSM 9
|||||

Db	1	HYGPGWVSM	9	
RESULT 2				
ABP74769				
ID	ABP74769	standard; peptide; 14 AA.		
XX				
AC	ABP74769;			
XX				
DT	03-FEB-2003	(first entry)		
XX				
DE		Proteome analysis related peptide #54.		
XX				
KW		Proteome analysis; isolation; determination; diagnostic assay; detection;		
KW		protein marker; identification; metastatic; invasive cancer;		
KW		differential expression; signalling pathway; chromatography.		
XX				
OS		Homo sapiens.		
OS		Synthetic.		
XX				
PN	WO200277016-A2.			
XX				
PD	03-OCT-2002.			
XX				
PF	22-MAR-2002; 2002WO-EP003368.			
XX				
PR	22-MAR-2001; 2001US-0278171P.			
PR	12-SEP-2001; 2001US-0318749P.			
PR	20-SEP-2001; 2001US-0323999P.			
XX				
PA	(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.			
XX				
PI	Vandekerckhove J, Gevaert K;			
XX				
DR	WPI; 2003-067379/06.			
XX				
PT		Method for isolation of peptides from complex mixture of peptides		
PT		involves specific chemical and/or enzymatic alteration of at least one		
PT		type of peptide.		
XX				
PS		Example 20; Page 141; 193pp; English.		
XX				
CC		The present invention describes a method (M1) for the isolation of a		
CC		subset of peptides from a protein peptide mixture (P1). M1 involves: (a)		
CC		separating the protein peptide mixture into fractions of peptides via		
CC		chromatography; (b) chemically, or enzymatically, or chemically and		
CC		enzymatically, altering at least one amino acid of at least one of the		
CC		peptides in each fraction, thereby generating a subset of altered		
CC		peptides; and (c) isolating the altered (flagged) peptides out of each		
CC		fraction via chromatography, where the chromatography of steps (a) and		
CC		(c) is performed with the same type of chromatography. M1 can be used for		
CC		the isolation and determination of peptides from protein peptide		
CC		mixtures. M1 can also be used in diagnostic assays for detection of the		
CC		presence, the absence or a variation in expression level of at least one		
CC		protein marker or a specific set of proteins indicative of a disease		
CC		state. M1 can be used for identifying target proteins present in		
CC		metastatic and invasive cancers, in differential expression of proteins		
CC		in transgenic mice, identification of proteins that are upregulated or		
CC		down regulated in disease tissues, in identification of intracellular		
CC		changes in cells with physiological changes such as metabolic shift, in		
CC		the identification of biomarkers in cancers and in the identification of		
CC		signalling pathways. The method is gel-free methodology for qualitative		
CC		and quantitative proteome analysis without the need for multidimensional		
CC		chromatography and without the use of affinity tags. ABP74714 to ABP75190		
CC		represent peptide sequences used in the exemplification of the present		
XX		invention		
SQ		Sequence 14 AA;		
		Query Match 100.0%; Score 58; DB 6; Length 14;		
		Best Local Similarity 100.0%; Pred. No. 0.0059;		
		Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	HYGPGWVSM	9	
Db	1	HYGPGWVSM	9	
RESULT 3				
AAAY69947				
ID	AAAY69947	standard; peptide; 10 AA.		
XX				
AC	AAAY69947;			
XX				
DT	11-APR-2000	(first entry)		
XX				
DE		Human cyclophilin B peptide fragment #27.		
XX				
KW		Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;		
KW		HLA antigen; diagnosis; tumour; therapy.		
XX				
OS		Homo sapiens.		
XX				
PN	WO9967288-A1.			
XX				
PD	29-DEC-1999.			
XX				
PF	24-JUN-1999; 99WO-JP003360.			
XX				
PR	25-JUN-1998; 98JP-00178449.			
XX				
PA	(SUMU) SUMITOMO PHARM CO LTD.			
PA	(ITOH/) ITOH K.			
XX				
PI	Itoh K, Gomi S;			
XX				
DR	WPI; 2000-116932/10.			
XX				
PT		Tumor antigen peptides derived from cyclophilin B for treatment and		
PT		diagnosis of tumors.		
XX				
PS		Claim 4; Page 56; 64pp; Japanese.		
XX				
CC		This sequence represents a cyclophilin B peptide of the invention. The		
CC		peptides are tumour antigen peptides derived from cyclophilin B, that		
CC		recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The		
CC		peptides are used for the treatment and diagnosis of tumours		
SQ		Sequence 10 AA;		
		Query Match 84.5%; Score 49; DB 3; Length 10;		
		Best Local Similarity 100.0%; Pred. No. 0.13;		
		Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	HYGPGWV	7	
Db	4	HYGPGWV	10	
RESULT 4				
ABR84352				
ID	ABR84352	standard; peptide; 10 AA.		
XX				
AC	ABR84352;			
XX				
DT	06-NOV-2003	(first entry)		
XX				
DE		Human CypB HLA-A2 epitope, SEQ ID NO:3.		
XX				
KW		Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;		
KW		cancer; tumour; cervical cancer; prostate cancer; cellular immunity;		
KW		immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;		
KW		human; human leukocyte antigen; HLA-A2 epitope.		
XX				
OS		Homo sapiens.		
XX				

PN JP2002365286-A.
 XX 18-DEC-2002.
 XX 18-SEP-2001; 2001JP-00283413.
 XX 13-NOV-2000; 2000JP-00345094.
 PR (ITOY/) ITO Y.
 XX WPI; 2003-508315/48.
 XX A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX Example 7; Page 8; 18pp; Japanese.
 XX The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention
 XX Sequence 10 AA;
 SQ Query Match 84.5%; Score 49; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGPGWV 7
 Db |||||
 4 HYGPGWV 10
 RESULT 5
 AAY69925
 ID AAY69925 standard; peptide; 11 AA.
 XX AAY69925;
 AC AAY69925;
 XX 11-APR-2000 (first entry)
 DT Human cyclophilin B peptide fragment #5.
 DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 XX HLA antigen; diagnosis; tumour; therapy.
 KW Homo sapiens.
 XX WO9967288-A1.
 PN 29-DEC-1999.
 PD 24-JUN-1999; 99WO-JP003360.
 XX 25-JUN-1998; 98JP-00178449.
 PR (SUMU) SUMITOMO PHARM CO LTD.
 XX (ITOY/) ITOH K.
 PA Itoh K, Gomi S;
 XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX Claim 4; Page 50; 64pp; Japanese.
 XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX Sequence 11 AA;
 SQ Query Match 77.6%; Score 45; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGPGW 6
 Db |||||
 6 HYGPGW 11
 RESULT 6
 AAR47787
 ID AAR47787 standard; protein; 14 AA.
 XX AAR47787;
 AC AAR47787;
 XX 25-MAR-2003 (revised)
 DT 27-JUL-1994 (first entry)
 DT HIV epitope #120.
 DE HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 XX outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 OS Human immunodeficiency virus.
 XX WO9402626-A1.
 PN 03-FEB-1994.
 PD 19-JUL-1993; 93WO-US006751.
 XX 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.
 XX (MERI) MERCK & CO INC.
 PA Keller PM, Conley AJ, Shaw AR, Arnold BA;
 XX WPI; 1994-048884/06.
 DR New conjugates for treating or preventing HIV infection - comprising HIV-
 XX specific neutralisation epitopes covalently linked to outer membrane
 PT proteosome of Neisseria.
 PT Claim 1; Page 151; 181pp; English.
 PS The sequences given in AAR47668-788 are HIV-specific selected principal
 XX neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)
 XX Sequence 14 AA;
 SQ

Query Match 58.6%; Score 34; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
Db 7 HYGP 11

RESULT 7
AAR95759
ID AAR95759 standard; peptide; 8 AA.
XX
AC AAR95759;
XX
DT 04-DEC-1996 (first entry)
XX
DE Alpha-4Beta-1 integrin binding inhibitory peptide 56.
XX
KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
KW inhibitor; binding; white blood cell; migration; capillary wall;
KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
KW CS1; CS5; H1; LDV; active site.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Pro-NH2"
FT
XX
PN US5510332-A.
XX
PD 23-APR-1996.
XX
PF 07-JUL-1994; 94US-00271830.
XX
PR 07-JUL-1994; 94US-00271830.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Beck PJ, Vanderslice P, Kogan TP, Ren K;
XX WPI; 1996-221274/22.
XX
PT New peptide(s) based on the LDV domain of fibronectin - used for
PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or
PT invasin.
XX
PS Claim 4; Col 43-44; 35pp; English.
XX
CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
CC surface of endothelial cells that line the interior wall of capillaries.
CC VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or VLA-
CC 4 for very late antigen-4), a heterodimeric protein present on the
CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
CC white blood cells to adhere to the capillary wall in areas where the
CC tissue surrounding the capillary has been infected or damaged. Sometimes
CC this white blood cell migration can become uncontrolled, with white blood
CC cells flooding to the scene, causing widespread tissue damage. Cpds.
CC capable of blocking this process may be beneficial as therapeutic agents.
CC IA4B1 also recognises the extracellular matrix glycoprotein fibronectin.
CC Three distinct IA4B1-binding sites have been identified within
CC fibronectin. One site is found in the HeplI region and is expressed in
CC all isoforms; two others (CS1 and CS5) are present in the alternatively
CC spliced type III connecting segments. CS1 has the higher affinity for
CC IA4B1 and contains the tripeptide LDV as its minimal active site.
CC Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that
CC include the LDV domain presented in such a way by its novel flanking
CC sequence to produce a potent inhibitor of IA4B1 binding.
XX
SQ Sequence 8 AA;

Query Match 55.2%; Score 32; DB 2; Length 8;

Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWVSM 9
Db 1 GPGWLDV 7

RESULT 8
AAR88101
ID AAR88101 standard; peptide; 8 AA.
XX
AC AAR88101;
XX
DT 22-JUL-1996 (first entry)
XX
DE Bovine p32 11-cis-retinol dehydrogenase tryptic fragment P322.
XX
KW Clone p-lambda-321; bovine; p32; 11-cis-retinol; dehydrogenase;
KW 11-cis-retinaldehyde; diagnosis; retinoid; retinitis pigmentosa;
KW psoriasis; acne; cancer; T-cell leukaemia; drug development; treatment;
KW retinal pigment epithelial cell; tryptic fragment; leukemia.
XX
OS Synthetic.
XX
PN WO9534580-A1.
XX
PD 21-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US006256.
XX
PR 10-JUN-1994; 94US-00258418.
PR 20-JAN-1995; 95US-00375962.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Hellman U, Wernstedt C, Eriksson U;
XX WPI; 1996-049624/05.
XX
PT Nucleic acid encoding a retinol dehydrogenase protein - used to develop
PT prods. for the diagnosis and treatment of retinoid-linked pathological
PT conditions.
XX
PS Example 4; Page 10; 35pp; English.
XX
CC Bovine p32 11-cis-retinol dehydrogenase, which catalyses the conversion
CC of 11-cis-retinol into 11-cis-retinaldehyde, can be used for the
CC diagnosis of retinoid linked pathological conditions, e.g. retinitis
CC pigmentosa, psoriasis, acne and certain cancers (i.e. T-cell leukaemias),
CC and for the development of drugs to treat these conditions. The p32 DNA
CC clone p-lambda-321 was isolated from bovine retinal pigment epithelial
CC (RPE) cell mRNA, using degenerate primers based on the 32 kD bovine RPE
CC cell derived protein p32 tryptic fragments AAR88100-04
XX
SQ Sequence 8 AA;

Query Match 53.4%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
Db 1 YSPGW 5

RESULT 9
AAW18339
ID AAW18339 standard; peptide; 8 AA.
XX
AC AAW18339;
XX
DT 18-AUG-1997 (first entry)

```
XX DE Bovine p32 11-cis-retinol dehydrogenase tryptic peptide p322.
XX DE
XX KW 11-Cis retinol dehydrogenase; p32; 11-cis retinaldehyde;
XX KW retinitis pigmentosa; psoriasis; acne; cancer; diagnosis; therapy.
XX OS
XX OS Bos taurus.
XX PN WO9719167-A1.
XX PD
XX PD 29-MAY-1997.
XX PF
XX PF 14-NOV-1996; 96WO-US018295.
XX PR
XX PR 22-NOV-1995; 95US-00562114.
XX PR 11-OCT-1996; 96US-00729594.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI
XX PI Eriksson U, Simon A, Romert A;
XX DR WPI; 1997-298106/27.
XX PT
XX PT New 11-cis retinol dehydrogenase gene - used to develop products for the
XX PT diagnosis and therapy of conditions such as retinitis pigmentosa,
XX PT psoriasis and cancers.
XX PS
XX PS Example 4; Page 11; 68pp; English.
XX CC
XX CC Tryptic peptides (AAW18338-42) were isolated from bovine retinal pigment
XX CC epithelial (RPE) membrane protein p32. PCR primers (see also AAT68946-49)
XX CC based on these primers were used to amplify cDNA (see also AAT68935)
XX CC coding for bovine p32 (AAW18343) from a RPE cDNA library. Peptide p322
XX CC corresponds to amino acids 281-288 of the p32 sequence deduced from the
XX CC cDNA clone. p32 is an 11-cis retinol dehydrogenase and forms a complex
XX CC with a component of the membrane receptor for retinol binding protein
XX SQ
XX SQ Sequence 8 AA;
XX Query Match 53.4%; Score 31; DB 2; Length 8;
XX Best Local Similarity 80.0%; Pred. No. 1.4e+06;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGPGW 6
Db | |||
1 YSPGW 5
RESULT 10
AAY01990
ID AAY01990 standard; peptide; 8 AA.
XX AC AAY01990;
XX DT 02-JUL-1999 (first entry)
XX DE
XX DE Tryptic peptide of bovine p32 protein.
XX KW
XX KW p32 protein; retinol dehydrogenase; 9-cis; 11-cis; 13-cis;
XX KW trans retinol dehydrogenase; oligomeric protein complex;
XX KW membrane receptor; retinol binding protein;
XX KW short chain alcohol dehydrogenase family; retinaldehyde;
XX KW retinitis pigmentosa; skin disorder; psoriasis; acne; T-cell leukemia.
XX OS
XX OS Bos sp.
XX PN WO9916788-A1.
XX PD
XX PD 08-APR-1999.
XX PF
XX PF 21-SEP-1998; 98WO-US019836.
XX XX
XX XX 26-SEP-1997; 97US-00937993.
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XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI
XX PI Eriksson U, Simon A, Romert A;
XX DR WPI; 1999-255059/21.
XX PT
XX PT New retinol dehydrogenase proteins, used to screen potential retinoid
XX PT drugs for treatment of various diseases, e.g. retinitis pigmentosa.
XX PS
XX PS Example 4; Page 14; 88pp; English.
XX CC
XX CC AAY01989-93 represent peptide obtained after tryptic digest of a p32
XX CC protein, isolated in the course of the invention. The specification
XX CC describes proteins having retinol dehydrogenase activity, such as 9-cis,
XX CC 11-cis, 13-cis, or trans retinol dehydrogenase activity. These proteins
XX CC form oligomeric protein complexes with the components of the membrane
XX CC receptor for retinol binding protein. The retinol dehydrogenase proteins
XX CC are members of the short chain alcohol dehydrogenase family. The
XX CC recombinant enzymes can be used to produce 9-cis and 11-cis
XX CC retinaldehydes. The proteins and nucleic acids encoding them can be used
XX CC to screen potential retinoid drugs for treatment of various diseases,
XX CC e.g. diseases of the eye such as retinitis pigmentosa and skin disorders
XX CC such as psoriasis and acne. Certain T-cell leukemias may also be tested
XX CC by retinoid drugs. Antibodies against the protein can be used to monitor
XX CC pathological conditions characterized by aberrant levels of a receptor
XX CC for retinol binding protein
XX SQ
XX SQ Sequence 8 AA;
XX Query Match 53.4%; Score 31; DB 2; Length 8;
XX Best Local Similarity 80.0%; Pred. No. 1.4e+06;
XX Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGPGW 6
Db | |||
1 YSPGW 5
RESULT 11
ABP46859
ID ABP46859 standard; peptide; 8 AA.
XX AC ABP46859;
XX DT 19-AUG-2002 (first entry)
XX DE
XX DE Human BLYS binding scFv VH CDR3 SEQ ID 2870.
XX KW
XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD
XX PD 10-JAN-2002.
XX PF
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
```

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 2; Page 3068; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 SQ Sequence 8 AA;

Query Match 51.7%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GPGW 6
 ||||
 Db 2 GPGW 5

RESULT 12
 AAP95363
 ID AAP95363 standard; peptide; 9 AA.
 XX
 AC AAP95363;
 XX
 DT 30-MAR-1992 (first entry)
 XX
 DE Variable region V3, found in the envelope protein gp120 of an AIDS or ARC
 DE causing or related virus strain MAL.
 XX
 KW Vaccine; AIDS; ARC; HIV; diagnosis.
 XX
 OS AIDS virus.
 XX
 PN EP311219-A.
 XX
 PD 12-APR-1989.
 XX
 PF 07-OCT-1988; 88EP-00202248.
 XX
 PR 09-OCT-1987; 87NL-00002403.
 XX
 PA (DIER-) STICHTING CENT DIER.
 PA (UNAM) UNIV VAN AMSTERDAM.
 PA (UYAM-) UNIV AMSTERDAM ZIEKENHUI.
 XX
 PI Goudsmit J, Meloen RH;
 XX
 DR WPI; 1989-108193/15.
 XX
 PT Oligopeptide(s) corresp. to beta-turn variable region of gp.120 - used
 PT for diagnosis of and prodn of vaccines against AIDS and ARC.
 XX
 PS Disclosure; Page 4; 7pp; English.

XX The peptides of the invention comprise the beta-turn AA SQ GPG or GPGR at
 CC positions 312-314 or 312-315 in the AA numbering of HTLV-IIIB (BH10) and
 CC flanking AA SQs having a length equal to or greater than 1 and pref.
 CC equal to or greater than 2 AAs; variants in which the GPG or GPGR SQ has
 CC been replaced by a different beta-turn SQ; and variants in which the free
 CC NH2-terminal gp AA and/or the free carboxyl terminal gp. AA has been
 CC blocked or modified otherwise
 XX
 SQ Sequence 9 AA;

Query Match 51.7%; Score 30; DB 1; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVGPG 5
 |:|||
 Db 2 HFGPG 6

RESULT 13
 AAR31288
 ID AAR31288 standard; peptide; 9 AA.
 XX
 AC AAR31288;
 XX
 DT 12-FEB-1993 (first entry)
 XX
 DE HIV principal determinant peptide.
 XX
 KW AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;
 KW meningitidis b; outer membrane protein complex; OMPC; PND-MAL.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "bonds to the OMPC of the conjugate via this site"

PN EP467700-A.
 XX
 PD 22-JAN-1992.
 XX
 PF 19-JUL-1991; 91EP-00306598.
 XX
 PR 19-JUL-1990; 90US-00555339.
 PR 19-JUL-1990; 90US-00555966.
 PR 19-JUN-1991; 91US-00715276.
 PR 19-JUN-1991; 91US-00715278.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Leanza WJ, Marburg S, Tolman RL, Emini EA;
 XX
 DR WPI; 1992-026505/04.
 XX
 PT Conjugate proteins comprising HIV peptide components - useful for
 PT preparing vaccines for e.g. AIDS or for treating infections.
 XX
 PS Claim 12; Page 56; 63pp; English.

XX The invention relates to a co-conjugate comprising an immunogenic protein
 CC or protein complex having a first set of covalent linkages to low
 CC molecular weight moieties which have an anionic or polyanionic character
 CC at physiological pH, and a second set of covalent linkages to peptides
 CC comprising HIV principal neutralizing determinants (PND's) or
 CC immunologically equivalent peptides. Preferably at least one set of the
 CC covalent linkages is comprised of maleimide derivatives; the
 CC (poly)anionic moiety is composed of one to five residues of the anionic
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
 CC protein is the outer membrane protein complex (OMPC) of Neisseria
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-

CC bonded cyclic structure. The present sequence (PND-MAL) is an example of
CC a PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX
SQ Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
|:|
Db 2 HFGPG 6

RESULT 14
AAR30043
ID AAR30043 standard; peptide; 9 AA.
XX
AC AAR30043;

XX 25-MAR-2003 (revised)
DT 28-APR-1993 (first entry)

XX HIV principle neutralising determinant MAL.

XX Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
KW major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
KW passive immunisation.

XX Human immunodeficiency virus.

XX EP519554-A1.

XX 23-DEC-1992.

XX 11-JUN-1992; 92EP-00201693.

XX 19-JUN-1991; 91US-00715273.

XX (MERI) MERCK & CO INC.

XX Emini A, Liu MA, Marburg S, Tolman RL;

XX WPI; 1992-425771/52.

XX Conjugates of HIV-1 PND peptide(s) with the MIEP of Neisseria
PT meningitidis - useful as a vaccine for treating and preventing HIV-1
PT infection, e.g. AIDS in humans.

XX Claim 9; Page 60; 66pp; English.

XX The peptide is HIV principle neutralising determinant (PND) MAL and is
CC used as part of a conjugate comprising the major immune enhancing protein
CC (MIEP) of Neisseria meningitidis covalently linked to the HIV PND. The
CC conjugate may be used to prepare vaccines against HIV infection, e.g.
CC AIDS, as research tools for studying PND structure- function
CC relationships, or as immunogens for use in the passive immunisation of
CC humans. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
|:|
Db 2 HFGPG 6

RESULT 15
AAR26724
ID AAR26724 standard; peptide; 9 AA.

XX AAR26724;

XX 09-FEB-1993 (first entry)

XX HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;
KW outer membrane protein complex; OMPC; Neisseria; AIDS; PND-MAL.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1
FT /note= "Joins onto polysaccharide-protein complex via
FT this site"

XX EP468714-A.

XX 29-JAN-1992.

XX 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555974.

XX 19-JUN-1991; 91US-00715275.

XX 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-034437/05.

XX HIV peptide-polysaccharide-protein conjugates - used in vaccines or to
PT produce antibodies to prevent or treat HIV infection.

XX Claim 9; Page 57; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing
CC determinant (PND), or an immunologically equivalent peptide (PEP),
CC covalently coupled to an immunogenic protein or protein complex through
CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.
CC The present sequence (PND-MAL) is an example of a PND peptide component.
CC The conjugates are used for inducing HIV-neutralising antibodies or for
CC making vaccines to prevent contraction of HIV infection or disease. The
CC antibodies can be used for passively protecting against infection by HIV,
CC or for protecting against proliferation of HIV post-infection, or for
CC treating AIDS, or in diagnostic assays

XX Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
|:|
Db 2 HFGPG 6

RESULT 16
AAU98826
ID AAU98826 standard; peptide; 11 AA.
XX
AC AAU98826;

DE HIV epitope #66.
 XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 XX Human immunodeficiency virus.
 OS
 XX WO9402626-A1.
 PN
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006751.
 XX
 PR 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX Keller PM, Conley AJ, Shaw AR, Arnold BA;
 PI
 XX WPI; 1994-048884/06.
 DR
 XX New conjugates for treating or preventing HIV infection - comprising HIV-
 PT specific neutralisation epitopes covalently linked to outer membrane
 PT proteosome of Neisseria.
 XX
 PS Claim 1; Page 124; 181pp; English.
 XX
 CC The sequences given in AAR47668-788 are HIV-specific selected principal
 CC neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)
 CC
 XX Sequence 13 AA;
 SQ
 Query Match 51.7%; Score 30; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGP 5
 Db |::|||
 4 HFGPG 8
 RESULT 19
 AAR47760
 ID AAR47760 standard; protein; 14 AA.
 XX
 AC AAR47760;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUL-1994 (first entry)
 XX
 DE HIV epitope #93.
 XX
 KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO9402626-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 19-JUL-1993; 93WO-US006751.

XX 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX Keller PM, Conley AJ, Shaw AR, Arnold BA;
 PI
 XX WPI; 1994-048884/06.
 DR
 XX New conjugates for treating or preventing HIV infection - comprising HIV-
 PT specific neutralisation epitopes covalently linked to outer membrane
 PT proteosome of Neisseria.
 XX
 PS Claim 1; Page 138; 181pp; English.
 XX
 CC The sequences given in AAR47668-788 are HIV-specific selected principal
 CC neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 51.7%; Score 30; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGP 5
 Db |::|||
 4 HFGPG 8
 RESULT 20
 ADD94624
 ID ADD94624 standard; peptide; 10 AA.
 XX
 AC ADD94624;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human SIMP-derived peptide 144.
 XX
 KW source of immunodominant MHC-associated peptide; SIMP; MHC;
 KW major histocompatibility complex; human leukocyte antigen; HLA;
 KW cytostatic; immunosuppressive; antisense therapy; gene therapy; cancer;
 KW lung cancer; intestine cancer; sarcoma; prostate cancer;
 KW testicular cancer; breast cancer; melanomas; pancreatic cancer;
 KW haematological cancer; immune response; lymphoid cell proliferation;
 KW autoimmune disease; transplant rejection; SIMP-derived peptide; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003054008-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 18-DEC-2002; 2002WO-CA001967.
 XX
 PR 20-DEC-2001; 2001US-00028384.
 XX
 XX (COMP-) COMPATIGENE INC.
 PA
 XX Perreault C, McBride K;
 PI
 XX WPI; 2003-559122/52.
 DR
 XX New human source of immunodominant MHC-associated peptide (SIMP) nucleic
 PT

PT acids and proteins, useful for diagnosing and treating cancers, e.g. lung
PT or breast cancer, or for suppressing an immune response in an autoimmune
PT disease.

Claim 24; Page 19; 66pp; English.

This invention relates to a novel isolated or purified human protein, termed source of immunodominant major histocompatibility complex (MHC) - associated peptide (SIMP), which is expressed ubiquitously in human cells, where the protein has the potential of generating several protein fragments binding with high affinity to a human leukocyte antigen (HLA) molecule. The invention may allow development of therapeutics with cytostatic or immunosuppressive activity or provide sequences useful for antisense therapy or gene therapy. The source of immunodominant MHC-associated peptide (SIMP) nucleic acids, proteins and fragments are useful for diagnosing and treating cancers, for example lung cancer, intestine cancer, sarcomas, prostate cancer, testicular cancer, breast cancer, melanomas, pancreatic cancer or haematological cancer. The SIMP proteins are also useful for modulating an immune response. Decreasing lymphoid cell proliferation is useful for suppressing an immune response responsible for an autoimmune disease or a transplant rejection. The present sequence is that of a human SIMP-derived peptide (with a high affinity binding motif for HLA molecules) of the invention.

Sequence 10 AA;

Query Match 50.0%; Score 29; DB 7; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
|:|
Db 5 HHGPG 9

RESULT 21

AAR47732
ID AAR47732 standard; protein; 14 AA.

XX AAR47732;

AC 25-MAR-2003 (revised)
DT 27-JUL-1994 (first entry)

XX HIV epitope #65.

KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;
KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
KW disease; antibody; human; monoclonal antibody; 447 antibody.

XX Human immunodeficiency virus.

XX WO9402626-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006751.

XX 20-JUL-1992; 92US-00917212.

XX 20-JUL-1992; 92US-00917214.

XX 20-JUL-1992; 92US-00917215.

XX 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

XX Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX WPI; 1994-048894/06.

PT New conjugates for treating or preventing HIV infection - comprising HIV-
PT specific neutralisation epitopes covalently linked to outer membrane
PT proteosome of Neisseria.

XX

PS

Claim 1; Page 124; 181pp; English.

XX

CC The sequences given in AAR47668-788 are HIV-specific selected principal
CC neutralisation epitopes which may be used in an antigenic conjugate
CC linked to purified outer membrane proteosome of Neisseria. This conjugate
CC may be used in an AIDS vaccine which may be used pre- and post-exposure
CC to prevent or treat HIV infection or disease. The vaccine is capable of
CC eliciting specific HIV neutralising antibodies and bind the broadly
CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
CC -2003 to correct PN field.)

XX Sequence 14 AA;

SQ

Query Match 50.0%; Score 29; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
|:|
Db 4 HHGPG 8

RESULT 22

AAM98717
ID AAM98717 standard; peptide; 14 AA.

XX AAM98717;

AC 24-JAN-2002 (first entry)

DT Human peptide #1992 encoded by a SNP oligonucleotide.

DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.

XX Disclosure; Page 4105; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX encoding polymorphic variants of proteins related to amylases, amyloid
XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX polymerase, oncogenes, histones, kinases, colony stimulating factors,
XX complement related proteins, cytochromes, kinesins, cytokines,
XX interferons, interleukins, G-protein coupled receptors and thioesterases.
XX The present sequence is a peptide encoded by one such oligonucleotide.
XX The oligonucleotides and the peptides encoded by them may be used in the
XX prevention, diagnosis and treatment of diseases associated with

CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX Sequence 14 AA;
SQ
Query Match 50.0%; Score 29; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 GPGWVS 8
Db ||| |:
8 GPWWIS 13
RESULT 23
ABB45010
ID ABB45010 standard; peptide; 8 AA.
XX
AC ABB45010;
XX
DT 06-FEB-2002 (first entry)
XX
DE Human albumin-binding peptide #59.
XX
KW Peptide ligand; immunoglobulin G; IgG; serum albumin; human.
XX
OS Synthetic.
XX WO200145746-A2.
PN
XX 28-JUN-2001.
PD
XX 22-DEC-2000; 2000WO-US035325.
PF
XX 23-DEC-1999; 99US-0173048P.
PR
XX (GETH) GENENTECH INC.
PA
XX Delano WL, Dennis MS, Lowman HB;
PI
XX WPI; 2001-514266/56.
DR
XX Peptide ligands with affinity for immunoglobulin (Ig) G, IgM and/or human
PT serum albumin which may be conjugated to, and used to prolong the
PT elimination half-time of active agents from the circulation.
XX
PS Example 6; Fig 5; 7lpp; English.
XX
CC The present invention relates to novel peptide ligands with affinity for
CC immunoglobulin (Ig) G or serum albumin. The peptide ligands may be
CC conjugated to, and used to prolong the elimination half-time of,
CC therapeutic and diagnostic agents in the body. The present sequence is a
CC human albumin-binding peptide used to illustrate the invention
XX
SQ Sequence 8 AA;
Query Match 48.3%; Score 28; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGWV 7
Db ||| |:
4 PGWV 7
RESULT 24
AAR76078
ID AAR76078 standard; peptide; 10 AA.

XX AAR76078;
AC
XX 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
DE Phage display peptide.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin; phage M13; phage display.
XX
OS Synthetic.
XX WO9515382-A1.
PN
XX 08-JUN-1995.
PD
XX 29-NOV-1994; 94WO-GB002610.
PF
XX 03-DEC-1993; 93GB-00024819.
PR
XX 03-JUN-1994; 94GB-00011089.
XX
PA (ZENE) ZENECA LTD.
XX
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
PI Blakey DC;
XX
DR WPI; 1995-215262/28.
XX
PT Antigen binding structures containing CDR's recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the diagnosis
PT and therapy of cancer.
XX
PS Claim 1; Page 96; 12lpp; English.
XX
CC An antigen binding structure (I) is based on the CDRs (given in AAR76078-
CC 84) of the heavy and light chains of MAb 55.1 (ECACC 93081901), which
CC recognises the colorectal tumor-associated antigen CA55.1. The peptide
CC given in AAR76078, as displayed on the surface of phage NCIMB 40638,
CC binds to (I) with an effective binding of 10 pM or less, and
CC competitively inhibits binding of (I) to Colo 205 cells (ATCC CCL 222).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HYGPGW 6
Db ||| |:
4 HRGSGW 9
RESULT 25
AAY31073
ID AAY31073 standard; peptide; 10 AA.
XX
AC AAY31073;
XX
DT 21-OCT-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 122.
XX
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers

FT Modified-site 1 /note= "pyroglutamic acid"
FT Modified-site 10 /note= "C-terminal amide"
XX US5945033-A.
XX 31-AUG-1999.
XX 12-NOV-1996; 96US-00747137.
XX 15-JAN-1991; 91US-00641720.
XX 13-OCT-1992; 92US-00959560.
XX 01-JUN-1993; 93US-00069831.
XX 14-MAR-1994; 94US-00212546.
XX (HEMO-) HEMOSPHERE INC.
XX Yen RCK;
XX WPI; 1999-508153/42.
XX Non-crosslinked protein particles for therapeutic and diagnostic use.
XX Example 22; Col 103-104; 65pp; English.
XX This invention describes a novel aqueous suspension of monodisperse
XX particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is
XX stable against dissolving upon dilution with an alcohol-free aqueous
XX medium. The method involves (a) forming an aqueous solution containing
XX albumin and hemoglobin and (b) treating the aqueous solution with an
XX alcohol to cause the solution to become turbid. The particles are useful
XX as agents for in vivo administration, either of their own administration
XX or as a vehicle for other therapeutic or diagnostic agents. The method
XX permits the formation of albumin and hemoglobin particles in the
XX nanometer and micrometer size range, in a form closer to their natural
XX form than the forms of the prior art. The particles therefore constitute
XX a more closely controlled agent for in vivo administration, with greater
XX ease of clearance from the body after their period of usefulness.
XX AAY30952-Y31135 represent peptides used in the method of the invention
SQ Sequence 10 AA;
Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HYGPGW 6
Db :: |||
3 NFSPGW 8
RESULT 26
ADC07128
ID ADC07128 standard; peptide; 10 AA.
XX
AC ADC07128;
XX
DT 18-DEC-2003 (first entry)
XX
DE Giant Madagascar hissing cockroach AKH peptide.
XX
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
KW obesity; type II diabetes; cholelithiasis; hypertension;
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
KW renal failure; liver; chronic pain; sleep apnea; stroke;
KW urinary incontinence; giant Madagascar hissing cockroach.
XX
OS Synthetic.
OS Gromphadorhina portentosa.
XX

FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "Pyroglutamic acid"
FT Misc-difference 10 /note= "Preferably C-terminal amide"
XX WO2003066080-A1.
XX 14-AUG-2003.
XX 07-FEB-2003; 2003WO-US003800.
XX 07-FEB-2002; 2002US-00072419.
XX (BLMB-) BLM GROUP.
XX Schacter BZ, Schacter LP;
XX WPI; 2003-712542/67.
XX Pharmaceutical composition useful for promoting weight loss, comprises an
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino
XX terminus.
XX Claim 29; Page 20; 82pp; English.
XX The invention relates to a novel method of promoting lipid mobilisation
XX in a human which comprises administering an insect adipokinetic hormone
XX (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
XX hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
XX hepatotropic, analgesic, cerebroprotective and uropathic activities. The
XX method of the invention may be useful for treating obesity, type II
XX diabetes, cholelithiasis, hypertension, coronary heart disease,
XX atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
XX failure, liver disease, chronic pain, sleep apnea, stroke and urinary
XX incontinence. The current sequence is that of the giant Madagascar
XX hissing cockroach AKH peptide of the invention.
SQ Sequence 10 AA;
Query Match 48.3%; Score 28; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HYGPGW 6
Db :: |||
3 NFSPGW 8
RESULT 27
AAW32655
ID AAW32655 standard; peptide; 12 AA.
XX
AC AAW32655;
XX
DT 30-JAN-1998 (first entry)
XX
DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
XX
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.
XX
OS Synthetic.
OS Homo sapiens.
XX WO9718236-A1.
XX
PD 22-MAY-1997.
XX
PF 08-NOV-1996; 96WO-US017882.

XX 13-NOV-1995; 95US-00556597.
 XX (UYNV) UNIV NEW YORK STATE RES FOUND.
 XX Miller JL, Lyle VA;
 XX WPI; 1997-289227/26.
 DR
 XX Peptide which mimics human platelet glycoprotein Ib/IX complex epitope -
 PT also anti-mimotope molecule capable of binding to the peptide and useful
 PT to modulate platelet adhesion, aggregation or agglutination.
 XX
 PS Claim 3; Page 97; 115pp; English.
 XX
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAB) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the MAB is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits the
 CC ristocetin induced aggregation of platelets
 XX
 SQ Sequence 12 AA;
 Query Match 48.3%; Score 28; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGWV 7
 Db :|||
 3 FGPFVW 8
 RESULT 28
 ID AAW71785 standard; peptide; 12 AA.
 XX AAW71785;
 AC
 XX 08-DEC-1998 (first entry)
 DT
 XX Mimotope capable of binding to monoclonal antibody C-34 #33.
 DE
 XX Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5817748-A.
 XX
 PD 06-OCT-1998.
 XX
 PF 17-MAR-1995; 95US-00406330.
 XX
 PR 17-MAR-1995; 95US-00406330.
 XX
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 XX
 XX Miller JL, Lyle VA;
 XX WPI; 1998-556458/47.
 DR
 XX Peptides that mimic platelet epitope - and neutralise aggregation-
 PT inhibiting antibody.
 XX
 PS Disclosure; Col 5; 26pp; English.

XX
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides AAW71752 to AAW71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be an
 CC antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic drugs.
 CC A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets through
 CC the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes
 XX
 SQ Sequence 12 AA;
 Query Match 48.3%; Score 28; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGWV 7
 Db :|||
 3 FGPFVW 8
 RESULT 29
 ID AAE27766 standard; peptide; 13 AA.
 XX AAE27766;
 AC
 XX 13-DEC-2002 (first entry)
 DT
 XX Human beta-glucocerebrosidase (beta-GCR) peptide #181.
 DE
 XX Human; fusion protein; immunological; major histocompatibility complex;
 KW MHC; nausea; gastric upset; beta-glucocerebrosidase; beta-GCR; enzyme;
 KW b-D-glucosyl-N-acylsphingosine glucosylase; E.C.3.2.1.45.
 XX
 OS Homo sapiens.
 XX
 PN WO200266514-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 18-FEB-2002; 2002WO-EP001690.
 XX
 PR 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 XX Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
 PI Hanlon M, Watkins J, Baker M, Way JC;
 PI
 XX WPI; 2002-667054/71.
 DR
 XX New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX
 PS Example 10; Page 61; 92pp; English.
 XX
 CC The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker

CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favourable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is human beta-glucocerebrosidase
CC (beta-GCR) peptide with potential major histocompatibility complex (MHC)
CC binding activity. The beta-GCR peptide is also referred to as b-D-
CC glucosyl-N-acylsphingosine glucosylase (E.C.3.2.1.45). This peptide is
CC used in the exemplification of the invention

XX SQ Sequence 13 AA;

Query Match 48.3%; Score 28; DB 5; Length 13;

Best Local Similarity 80.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWV 7

|||

8 GPNWV 12

RESULT 30

AAR47734

ID AAR47734 standard; protein; 14 AA.

XX AC AAR47734;

DT 25-MAR-2003 (revised)

DT 27-JUL-1994 (first entry)

XX DE HIV epitope #67.

XX KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;

XX KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;

XX KW disease; antibody; human; monoclonal antibody; 447 antibody.

XX OS Human immunodeficiency virus.

XX PN WO9402626-A1.

XX PD 03-FEB-1994.

XX PF 19-JUL-1993; 93WO-US006751.

XX PR 20-JUL-1992; 92US-00917212.

XX PR 20-JUL-1992; 92US-00917214.

XX PR 20-JUL-1992; 92US-00917215.

XX PR 20-JUL-1992; 92US-00917217.

XX PA (MERI) MERCK & CO INC.

XX PI Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX DR WPI; 1994-048884/06.

XX PT New conjugates for treating or preventing HIV infection - comprising HIV-

XX PT specific neutralisation epitopes covalently linked to outer membrane

XX PT proteosome of Neisseria.

XX PS Claim 1; Page 125; 181pp; English.

XX CC The sequences given in AAR47668-788 are HIV-specific selected principal

XX CC neutralisation epitopes which may be used in an antigenic conjugate

XX CC linked to purified outer membrane proteosome of Neisseria. This conjugate

XX CC may be used in an AIDS vaccine which may be used pre- and post-exposure

XX CC to prevent or treat HIV infection or disease. The vaccine is capable of

XX CC eliciting specific HIV neutralising antibodies and bind the broadly

XX CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR

XX CC -2003 to correct PN field.)

XX SQ Sequence 14 AA;

Query Match 48.3%; Score 28; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 4

||||

Db 4 HYGP 7

RESULT 31

AAR47770

ID AAR47770 standard; protein; 14 AA.

XX AC AAR47770;

DT 25-MAR-2003 (revised)

DT 27-JUL-1994 (first entry)

XX DE HIV epitope #103.

XX KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;

XX KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;

XX KW disease; antibody; human; monoclonal antibody; 447 antibody.

XX OS Human immunodeficiency virus.

XX PN WO9402626-A1.

XX PD 03-FEB-1994.

XX PF 19-JUL-1993; 93WO-US006751.

XX PR 20-JUL-1992; 92US-00917212.

XX PR 20-JUL-1992; 92US-00917214.

XX PR 20-JUL-1992; 92US-00917215.

XX PR 20-JUL-1992; 92US-00917217.

XX PA (MERI) MERCK & CO INC.

XX PI Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX DR WPI; 1994-048884/06.

XX PT New conjugates for treating or preventing HIV infection - comprising HIV-

XX PT specific neutralisation epitopes covalently linked to outer membrane

XX PT proteosome of Neisseria.

XX PS Claim 1; Page 143; 181pp; English.

XX CC The sequences given in AAR47668-788 are HIV-specific selected principal

XX CC neutralisation epitopes which may be used in an antigenic conjugate

XX CC linked to purified outer membrane proteosome of Neisseria. This conjugate

XX CC may be used in an AIDS vaccine which may be used pre- and post-exposure

XX CC to prevent or treat HIV infection or disease. The vaccine is capable of

XX CC eliciting specific HIV neutralising antibodies and bind the broadly

XX CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR

XX CC -2003 to correct PN field.)

XX SQ Sequence 14 AA;

Query Match 48.3%; Score 28; DB 2; Length 14;

Best Local Similarity 80.0%; Pred. No. 5.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5

:|||

Db 4 YGPG 8

RESULT 32

AAY57711

ID AAY57711 standard; peptide; 14 AA.

XX AC AAY57711;

XX 14-MAR-2000 (first entry)
DT
XX
DE Rat clusterin 47 kDa peptide.
XX
KW Clusterin; immunosuppressant; organ rejection; tissue transplantation;
KW autoimmune disease; inflammatory disease; rheumatism; atopy;
KW systemic erythematosis; allergy; hay fever.
XX
OS Rattus sp.
XX
XX WO9962541-A1.
PN
XX
PD 09-DEC-1999.
XX
XX 13-MAY-1999; 99WO-JP002474.
PF
XX
XX 01-JUN-1998; 98JP-00151570.
PR
XX (HISM) HISAMITSU PHARM CO LTD.
PA
XX Yuda K, Akiyama K, Goto T, Goto S;
PI
XX WPI; 2000-072735/06.
DR
XX
XX Immunosuppressants with reduced side-effects, useful for preventing
PT rejection in organ and tissue transplant and as remedies for autoimmune
PT diseases and inflammatory diseases (claimed) e.g. allergy.
PT
XX
PS Example 3; Page 12; 28pp; Japanese.
XX
CC The present invention describes an immunosuppressant which contains a
CC clusterin. The present sequence represents a rat clusterin peptide from
CC an example of the present invention. Also described is a method for
CC treating rejection in organ and tissue transplant, autoimmune diseases or
CC inflammatory diseases by administering an effective dose of the
CC immunosuppressant. The immunosuppressants are useful for preventing
CC rejection in organ and tissue transplant, particularly of heart, liver,
CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as
CC remedies for autoimmune diseases such as rheumatism, atopy, systemic
CC erythematosis, and inflammatory diseases including allergy such as hay
CC fever. The drugs are efficacious, with little side-effects
XX
SQ Sequence 14 AA;
Query Match 48.3%; Score 28; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYGP 4
Db 7 HYGP 10
RESULT 33
ABG66144
ID ABG66144 standard; peptide; 13 AA.
XX
AC ABG66144;
XX
DT 29-AUG-2002 (first entry)
XX
DE Ige Fcepsilon RI binding peptide from phage displayed library #1.
XX
KW Ige receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
KW protein co-ordinate data; Ige-mediated disease; allergic rhinitis;
KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
KW parasitic infection; Ige myeloma; immune-related disorder;
KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
KW Ige-mediated gastrointestinal inflammatory disease; burn;
KW immune rejection of graft; myocardial infarction; atherosclerosis;
KW acute lung injury; haemorrhagic shock; septic shock;
KW acute tubular necrosis; endometriosis; degenerative joint disease;

KW pancreatitis.
XX
XX Synthetic.
OS
XX WO200226781-A2.
PN
XX 04-APR-2002.
PD
XX 26-SEP-2001; 2001WO-US030289.
PF
XX 26-SEP-2000; 2000US-0235353P.
PR 23-MAR-2001; 2001US-0278540P.
XX
XX (GETH) GENENTECH INC.
PA
XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
PI
XX WPI; 2002-444016/47.
XX
DR
XX
PT A peptide useful for treating a Ige-mediated disease or disorder in a
PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
PT for binding to high affinity Ige receptor in an in vitro assay.
PT
XX
PS Example 6; Page 97; 328pp; English.
XX
CC The invention relates to a peptide which competes with immunoglobulin
CC (Ig) E 134 comprising a sequence (S1), for binding the high affinity Ige
CC receptor (FcepsilonRI) in an in vitro assay and having a formula given in
CC the specification. Also included are a fusion protein comprising the
CC peptide, a pharmaceutical composition (C) comprising the peptide,
CC designing a compound that mimics the three-dimensional surface structure
CC of the peptide, a compound with a solvent accessible surface that mimics
CC the solvent accessible surface defined by the side chains of residues (R)
CC Pro4, Phe6, Prol6, Cys3, Cys7, Cys15 and Cys19 of IgeE134, a peptide with
CC structural coordinates as given in the specification, selecting a peptide
CC mimetic which binds to FcepsilonRI and blocks binding of Ige and a
CC peptide mimetic which mimics the coordinates of IgeE134 residues (R). (C)
CC is useful for inhibiting the binding of Ige to high affinity Ige receptor
CC (FcepsilonRI). Peptides of the formula given in the specification are
CC useful for inhibiting the binding of an Ige to high affinity Ige
CC receptor. The peptide is useful for selecting a molecule which blocks the
CC interaction of Ige with high affinity Ige receptor. The peptide is also
CC useful for inhibiting the activation of high affinity Ige receptor. The
CC peptide is useful for treating an Ige-mediated disease or disorder in a
CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
CC methods. The peptide is also useful for inhibiting Ige-mediated or
CC associated processes such as Ige- dependent activation and degranulation
CC of mast cells and basophils, as well as consequent release of
CC inflammatory mediators such as histamine. (C) is useful for treating
CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
CC urticaria-angioedema, parasitic infection, Ige myeloma, immune-related
CC disorders, inflammatory disorders, diabetes mellitus, Ige-mediated
CC gastrointestinal inflammatory disease, immune rejection of grafts,
CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
CC present sequence is a peptide of the invention expressed from a phage
CC display library
XX
SQ Sequence 13 AA;
Query Match 47.4%; Score 27.5; DB 5; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3 GP-GWVSM 9
Db 6 GPWGWVCM 13
RESULT 34
ABG66104
ID ABG66104 standard; peptide; 13 AA.

XX ABG66104;
AC
XX 29-AUG-2002 (first entry)
DT
XX IGE Fcepsilon RI binding peptide from phage displayed g8 library IGE69.
DE
XX IGE receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
KW protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
KW parasitic infection; IGE myeloma; immune-related disorder;
KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
KW IGE-mediated gastrointestinal inflammatory disease; burn;
KW immune rejection of graft; myocardial infarction; atherosclerosis;
KW acute lung injury; haemorrhagic shock; septic shock;
KW acute tubular necrosis; endometriosis; degenerative joint disease;
KW pancreatitis.
XX
OS Synthetic.
XX
XX WO200226781-A2.
PN
XX
XX 04-APR-2002.
PD
XX 26-SEP-2001; 2001WO-US030289.
XX
XX 26-SEP-2000; 2000US-0235353P.
PR
XX 23-MAR-2001; 2001US-0278540P.
PR
XX (GETH) GENENTECH INC.
XX
XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
PI
XX WPI; 2002-444016/47.
DR
XX
XX A peptide useful for treating a IGE-mediated disease or disorder in a
PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
PT for binding to high affinity IGE receptor in an in vitro assay.
PT
XX
PS Example 4; Page 87; 328pp; English.
XX
XX The invention relates to a peptide which competes with immunoglobulin
CC (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
CC receptor (FcepsilonRI) in an in vitro assay and having a formula given in
CC the specification. Also included are a fusion protein comprising the
CC peptide, a pharmaceutical composition (C) comprising the peptide,
CC designing a compound that mimics the three-dimensional surface structure
CC of the peptide, a compound with a solvent accessible surface that mimics
CC the solvent accessible surface defined by the side chains of residues (R)
CC Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134, a peptide with
CC structural coordinates as given in the specification, selecting a peptide
CC mimetic which binds to FcepsilonRI and blocks binding of IGE and a
CC peptide mimetic which mimics the coordinates of IGE134 residues (R). (C)
CC is useful for inhibiting the binding of IGE to high affinity IGE receptor
CC (FcepsilonRI). Peptides of the formula given in the specification are
CC useful for inhibiting the binding of an IGE to high affinity IGE
CC receptor. The peptide is useful for selecting a molecule which blocks the
CC interaction of IGE with high affinity IGE receptor. The peptide is also
CC useful for inhibiting the activation of high affinity IGE receptor. The
CC peptide is useful for treating an IGE-mediated disease or disorder in a
CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
CC methods. The peptide is also useful for inhibiting IGE-mediated or
CC associated processes such as IGE-dependent activation and degranulation
CC of mast cells and basophils, as well as consequent release of
CC inflammatory mediators such as histamine. (C) is useful for treating
CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
CC urticaria-angioedema, parasitic infection, IGE myeloma, immune-related
CC disorders, inflammatory disorders, diabetes mellitus, IGE-mediated
CC gastrointestinal inflammatory disease, immune rejection of grafts,
CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
CC present sequence is a peptide of the invention expressed from a phage

CC display library
XX
SQ Sequence 13 AA;

Query Match 47.4%; Score 27.5; DB 5; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 GP-GWVSM 9
Db |||||
6 GPWGWWCM 13

RESULT 35
ABG66135
ID ABG66135 standard; peptide; 14 AA.
XX
XX AC ABG66135;
XX
XX 29-AUG-2002 (first entry)
DT
XX IGE Fcepsilon RI binding peptide from phage displayed g8 library IGE107.
DE
XX IGE receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
KW protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
KW parasitic infection; IGE myeloma; immune-related disorder;
KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
KW IGE-mediated gastrointestinal inflammatory disease; burn;
KW immune rejection of graft; myocardial infarction; atherosclerosis;
KW acute lung injury; haemorrhagic shock; septic shock;
KW acute tubular necrosis; endometriosis; degenerative joint disease;
KW pancreatitis.
XX
XX Synthetic.
XX
XX WO200226781-A2.
PN
XX
XX 04-APR-2002.
PD
XX
XX 26-SEP-2001; 2001WO-US030289.
PF
XX
XX 26-SEP-2000; 2000US-0235353P.
PR
XX 23-MAR-2001; 2001US-0278540P.
PR
XX (GETH) GENENTECH INC.
PA
XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
PI
XX WPI; 2002-444016/47.
DR
XX
XX A peptide useful for treating a IGE-mediated disease or disorder in a
PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
PT for binding to high affinity IGE receptor in an in vitro assay.
PT
XX
XX Example 4; Page 88; 328pp; English.
XX
XX The invention relates to a peptide which competes with immunoglobulin
CC (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
CC receptor (FcepsilonRI) in an in vitro assay and having a formula given in
CC the specification. Also included are a fusion protein comprising the
CC peptide, a pharmaceutical composition (C) comprising the peptide,
CC designing a compound that mimics the three-dimensional surface structure
CC of the peptide, a compound with a solvent accessible surface that mimics
CC the solvent accessible surface defined by the side chains of residues (R)
CC Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134, a peptide with
CC structural coordinates as given in the specification, selecting a peptide
CC mimetic which binds to FcepsilonRI and blocks binding of IGE and a
CC peptide mimetic which mimics the coordinates of IGE134 residues (R). (C)
CC is useful for inhibiting the binding of IGE to high affinity IGE receptor
CC (FcepsilonRI). Peptides of the formula given in the specification are
CC useful for inhibiting the binding of an IGE to high affinity IGE
CC receptor. The peptide is useful for selecting a molecule which blocks the

CC interaction of IgE with high affinity IgE receptor. The peptide is also
 CC useful for inhibiting the activation of high affinity IgE receptor. The
 CC peptide is useful for treating an IgE-mediated disease or disorder in a
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
 CC methods. The peptide is also useful for inhibiting IgE-mediated or
 CC associated processes such as IgE-dependent activation and degranulation
 CC of mast cells and basophils, as well as consequent release of
 CC inflammatory mediators such as histamine. (C) is useful for treating
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
 CC urticaria-angioedema, parasitic infection, IgE myeloma, immune-related
 CC disorders, inflammatory disorders, diabetes mellitus, IgE-mediated
 CC gastrointestinal inflammatory disease, immune rejection of grafts,
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
 CC present sequence is a peptide of the invention expressed from a phage
 CC display library

XX
 SQ Sequence 14 AA;

Query Match 47.4%; Score 27.5; DB 5; Length 14;
 Best Local Similarity 75.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 GP-GWVSM 9
 || || || ||
 Db 7 GPWGWVCM 14

RESULT 36

ABG66084
 ID ABG66084 standard; peptide; 14 AA.

AC ABG66084;

DT 29-AUG-2002 (first entry)

DE IgE Fcεpsilon RI binding peptide from phage displayed g3 library #14.

XX IgE receptor; immunoglobulin; FcεpsilonRI; antagonist; phage display;
 KW protein co-ordinate data; IgE-mediated disease; allergic rhinitis;
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
 KW parasitic infection; IgE myeloma; immune-related disorder;
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KW IgE-mediated gastrointestinal inflammatory disease; burn;
 KW immune rejection of graft; myocardial infarction; atherosclerosis;
 KW acute lung injury; haemorrhagic shock; septic shock;
 KW acute tubular necrosis; endometriosis; degenerative joint disease;
 KW pancreatitis.

XX Synthetic.

OS WO200226781-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US030289.

XX 26-SEP-2000; 2000US-0235353P.

PR 23-MAR-2001; 2001US-0278540P.

XX (GETH) GENENTECH INC.

XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;

XX WPI; 2002-444016/47.

XX A peptide useful for treating a IgE-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
 PT for binding to high affinity IgE receptor in an in vitro assay.

XX Example 3; Page 83; 328pp; English.

PS

CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (SI), for binding the high affinity IgE
 CC receptor (FcεpsilonRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface structure
 CC of the peptide, a compound with a solvent accessible surface that mimics
 CC the solvent accessible surface defined by the side chains of residues (R)
 CC Pro4, Phe6, Prol6, Cys3, Cys7, Cys15 and Cys19 of IgE134, a peptide with
 CC structural coordinates as given in the specification, selecting a peptide
 CC mimetic which binds to FcεpsilonRI and blocks binding of IgE and a
 CC peptide mimetic which mimics the coordinates of IgE134 residues (R). (C)
 CC is useful for inhibiting the binding of IgE to high affinity IgE receptor
 CC (FcεpsilonRI). Peptides of the formula given in the specification are
 CC useful for inhibiting the binding of an IgE to high affinity IgE
 CC receptor. The peptide is useful for selecting a molecule which blocks the
 CC interaction of IgE with high affinity IgE receptor. The peptide is also
 CC useful for inhibiting the activation of high affinity IgE receptor. The
 CC peptide is useful for treating an IgE-mediated disease or disorder in a
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
 CC methods. The peptide is also useful for inhibiting IgE-mediated or
 CC associated processes such as IgE-dependent activation and degranulation
 CC of mast cells and basophils, as well as consequent release of
 CC inflammatory mediators such as histamine. (C) is useful for treating
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
 CC urticaria-angioedema, parasitic infection, IgE myeloma, immune-related
 CC disorders, inflammatory disorders, diabetes mellitus, IgE-mediated
 CC gastrointestinal inflammatory disease, immune rejection of grafts,
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
 CC present sequence is a peptide of the invention expressed from a phage
 CC display library

XX
 SQ Sequence 14 AA;

Query Match 47.4%; Score 27.5; DB 5; Length 14;

Best Local Similarity 75.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 GP-GWVSM 9
 || || || ||

Db 4 GPWGWVCM 11

RESULT 37

ABG66103

ID ABG66103 standard; peptide; 14 AA.

XX AC ABG66103;

XX 29-AUG-2002 (first entry)

DE IgE Fcεpsilon RI binding peptide from phage displayed g8 library IGE68.

XX IgE receptor; immunoglobulin; FcεpsilonRI; antagonist; phage display;
 KW protein co-ordinate data; IgE-mediated disease; allergic rhinitis;
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
 KW parasitic infection; IgE myeloma; immune-related disorder;
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KW IgE-mediated gastrointestinal inflammatory disease; burn;
 KW immune rejection of graft; myocardial infarction; atherosclerosis;
 KW acute lung injury; haemorrhagic shock; septic shock;
 KW acute tubular necrosis; endometriosis; degenerative joint disease;
 KW pancreatitis.

XX Synthetic.

XX WO200226781-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US030289.

PF

XX 26-SEP-2000; 2000US-0235353P.
PR 23-MAR-2001; 2001US-0278540P.
XX (GETH) GENENTECH INC.
PA Lowman HB, Reynolds ME, Nakamura GR, Starovaasnik MA;
XX WPI; 2002-444016/47.
XX A peptide useful for treating a IGE-mediated disease or disorder in a
PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
PT for binding to high affinity IGE receptor in an in vitro assay.
XX Example 4; Page 87; 328pp; English.
PS The invention relates to a peptide which competes with immunoglobulin
XX (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
CC receptor (FcεpsilonRI) in an in vitro assay and having a formula given in
CC the specification. Also included are a fusion protein comprising the
CC peptide, a pharmaceutical composition (C) comprising the peptide,
CC designing a compound that mimics the three-dimensional surface structure
CC of the peptide, a compound with a solvent accessible surface that mimics
CC the solvent accessible surface defined by the side chains of residues (R)
CC Pro4, Phe6, Pro16, Cys7, Cys15 and Cys19 of IGE134, a peptide with
CC structural coordinates as given in the specification, selecting a peptide
CC mimetic which binds to FcεpsilonRI and blocks binding of IGE and a
CC peptide mimetic which mimics the coordinates of IGE134 residues (R). (C)
CC is useful for inhibiting the binding of IGE to high affinity IGE receptor
CC (FcεpsilonRI). Peptides of the formula given in the specification are
CC useful for inhibiting the binding of an IGE to high affinity IGE
CC receptor. The peptide is useful for selecting a molecule which blocks the
CC interaction of IGE with high affinity IGE receptor. The peptide is also
CC useful for inhibiting the activation of high affinity IGE receptor. The
CC peptide is useful for treating an IGE-mediated disease or disorder in a
CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
CC methods. The peptide is also useful for inhibiting IGE-mediated or
CC associated processes such as IGE-dependent activation and degranulation
CC of mast cells and basophils, as well as consequent release of
CC inflammatory mediators such as histamine. (C) is useful for treating
CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
CC urticaria-angioedema, parasitic infection, IGE myeloma, immune-related
CC disorders, inflammatory disorders, diabetes mellitus, IGE-mediated
CC gastrointestinal inflammatory disease, immune rejection of grafts,
CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
CC present sequence is a peptide of the invention expressed from a phage
CC display library
XX
SQ Sequence 14 AA;
Query Match 47.4%; Score 27.5; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3 GP-GWVSM 9
Db |||||
7 GPWGWVCM 14
RESULT 38
AAE34589
ID AAE34589 standard; peptide; 8 AA.
XX AAE34589;
AC AAE34589;
XX 14-MAY-2003 (first entry)
DT Phage peptide #4 from CL6 library.
XX
DE CERVIG protein; signal regulatory protein; autoimmune syndrome;
XX SIRPalpa; inflammation; urinary disease; central nervous system disease;
KW
KW

KW immune disease; gastrointestinal tract disease; TH1-type immune response;
KW graft versus host disease; pulmonary disease; RBC destruction; memory;
KW autoimmune haemolytic anaemia; gene therapy; nephrotropic; neurotropic;
KW immunosuppressive.
XX Unidentified.
OS WO200292784-A2.
XX 21-NOV-2002.
PD 15-MAY-2002; 2002WO-US018531.
XX 15-MAY-2001; 2001US-0291050P.
PR (UYEM-) UNIV EMORY.
XX Parkos CA;
XX WPI; 2003-120676/11.
XX New isolated CERVIG polypeptide, useful for modulating SIRPalpa-CD47
PT functions and in treating conditions such as inflammation, graft versus
PT host disease and autoimmune syndromes.
XX Example 1; Page 45; 104pp; English.
PS The invention relates to CERVIG proteins and polynucleotides encoding
XX such proteins. Sequences of the invention are useful in modulating signal
CC regulatory proteins (SIRP)alpha-CD47 functions and in treating conditions
CC such as inflammation, pulmonary diseases, urinary diseases, central
CC nervous system diseases, immune diseases and gastrointestinal tract
CC diseases. They are particularly used to inhibit the development of TH1-
CC type immune response, undesirable effects of graft versus host disease
CC and autoimmune syndromes, inhibit inappropriate RBC destruction in
CC autoimmune haemolytic anaemia or related diseases and improve memory.
CC CERVIG sequences are also used in gene therapy. The present sequence is a
CC phage peptide used in the exemplification of the invention
XX Sequence 8 AA;
SQ
Query Match 46.6%; Score 27; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HVGPGW 6
Db |||||
2 HPGTGW 7
RESULT 39
AAB70713
ID AAB70713 standard; peptide; 9 AA.
XX AAB70713;
AC AAB70713;
XX 14-MAY-2001 (first entry)
DT Human TAA R11 immunogenic peptide fragment SEQ ID 38.
XX TAA; tumor associated antigen; R11; immunogenic; anticancer; vaccine;
KW cellular immune response; humoral immune response; cancer cell;
KW immunotherapy; cancer; cytostatic agent; breast carcinoma; diagnosis;
KW adrenal carcinoma; pancreatic carcinoma.
XX Homo sapiens.
OS DE19936563-A1.
XX 08-FEB-2001.
PD 04-AUG-1999; 99DE-01036563.
XX

PR 04-AUG-1999; 99DE-01036563.
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA Konopitzky R, Koenig U, Sommergruber W, Woelfel T;
PI WPI; 2001-203694/21.
XX New tumor-associated antigen R11, useful for immunotherapy of tumors and
PT for diagnosis, e.g. to assess the immune response to vaccination or for
PT prognosis of tumors.
XX Claim 5; Page 32; 46pp; German.
PS This invention describes a novel tumor-associated antigen designated R11
XX comprising a 356 amino acid (aa) sequence, as defined in the
CC specification. The invention also describes (a) immunogenic protein
CC fragments or peptides (I) derived from R11; (b) isolated DNA (II)
CC encoding a protein (III) with the immunogenic properties of R11, and its
CC fragments; (c) recombinant DNA that includes (II); and (d) antibodies
CC (Ab) directed against R11 or (I). The products of the invention have
CC anticancer activity and induce specific cellular or humoral immune
CC response against cancer cells. R11, or derived immunogenic peptides and
CC (recombinant) nucleic acid encoding them, are used for in vitro or in
CC vivo immunotherapy of cancers. Cells that express R11 are useful in
CC cancer vaccines and antibodies (Ab) that recognize R11 are used for
CC treatment (e.g. when coupled to a cytostatic agent or radioisotope),
CC diagnosis or monitoring of cancers associated with expression of R11
CC (particularly breast, adrenal or pancreatic carcinoma). R11-derived
CC peptides can also be used for diagnosis, e.g. to assess the immune
CC response to vaccination or for prognosis of tumors
XX Sequence 9 AA;
SQ Query Match 46.6%; Score 27; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 GPGWVS 8
DB 3 GPRWLS 8
RESULT 40
AAR31271
ID AAR31271 standard; peptide; 10 AA.
XX AAR31271;
AC AAR31271;
XX 12-FEB-1993 (first entry)
DT HIV principal determinant peptide.
DE AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
KW meningitidis b; outer membrane protein complex; OMPC; cPND30.
XX Synthetic.
OS Key Location/Qualifiers
FH Modified-site 1 /label= Nle
FT /note= "this position is linked to the OMPC of the
FT conjugate"
FT Modified-site 2
FT /note= "epsilon-amino group is condensed with C-terminal
FT COOH to form cyclic peptide"
FT Modified-site 10
FT /note= "forms amide bond with epsilon-amino of Lys(2) to
FT give cyclic molecule"
XX EP467700-A.
PN 22-JAN-1992.
XX

XX 19-JUL-1991; 91EP-00306598.
PF 19-JUL-1990; 90US-00555339.
XX 19-JUL-1990; 90US-00555966.
PR 19-JUN-1991; 91US-00715276.
PR 19-JUN-1991; 91US-00715278.
XX (MERI) MERCK & CO INC.
PA Leanza WJ, Marburg S, Tolman RL, Emini EA;
XX WPI; 1992-026505/04.
XX Conjugate proteins comprising HIV peptide components - useful for
PT preparing vaccines for e.g. AIDS or for treating infections.
PS Claim 12; Page 55; 63pp; English.
XX The invention relates to a co-conjugate comprising an immunogenic protein
CC or protein complex having a first set of covalent linkages to low
CC molecular weight moieties which have an anionic or polyanionic character
CC at physiological pH, and a second set of covalent linkages to peptides
CC comprising HIV principal neutralizing determinants (PND's) or
CC immunologically equivalent peptides. Preferably at least one set of the
CC covalent linkages is comprised of maleimide derivatives; the
CC (poly)anionic moiety is composed of one to five residues of the anionic
CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
CC protein is the outer membrane protein complex (OMPC) of Neisseria
CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
CC bonded cyclic structure. The present sequence (cPND30) is an example of a
CC PND peptide component used in the co-conjugate. The co-conjugate is
CC useful for inducing anti-peptide immune response in mammals, for inducing
CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
CC prevent HIV infection or disease, including AIDS, or for treating humans
CC afflicted with HIV infection or disease
XX Sequence 10 AA;
SQ Query Match 46.6%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HYGPGWV 7
DB 3 HIGPGRV 9
RESULT 41
AAR31308
ID AAR31308 standard; peptide; 10 AA.
XX AAR31308;
AC AAR31308;
XX 11-FEB-1993 (first entry)
DT Cyclic HIV principal neutralizing determinant peptide.
DE Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; vaccine;
XX immunogen; ELISA; analysis; cPND30.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /label= Nle
FT /note= "Z-Nle"
FT Modified-site 2
FT /note= "forms cyclic lactam bond, via epsilon-NH2, with C
FT -terminal COOH"
FT Modified-site 10
FT /note= "forms cyclic amide bond with epsilon- NH2 of
FT

FT XX Lys(2) "

PN EP471453-A.

XX 19-FEB-1992.

PD 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

PF (MERI) MERCK & CO INC.

XX Sugg BE, Dolan CA, Bednarek MA, Tolman RL, Christense BG;

XX WPI; 1992-058511/08.

DR New cyclic HIV principal neutralising determinant peptide(s) - used as

XX laboratory tools and as vaccines against HIV, AIDS, arc etc.

PS Claim 4; Page 22; 25pp; English.

XX The peptide (cPND30) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims

CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result

CC of a lactam bridge between an NH2 on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.

CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND

CC peptides (cPND's) may be used as analytical tools and as reagents in

CC ELISA assays. They may also be conjugated to an immunogenic carrier (a

CC protein and/or a polysaccharide; e.g. PRP or OMPC) to give a product

CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing

CC immune responses and for formulating vaccines to prevent HIV disease,

CC including AIDS and ARC, or for treating humans afflicted with HIV disease

CC such as AIDS or ARC

XX SQ Sequence 10 AA;

Query Match 46.6%; Score 27; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7

Db 3 HIGPGRV 9

RESULT 42

AAR26707

ID AAR26707 standard; peptide; 10 AA.

AC AAR26707;

XX 09-FEB-1993 (first entry)

DT HIV-PND-polysaccharide-protein conjugate vaccine.

DE Human immunodeficiency virus; principal neutralizing determinant;

XX outer membrane protein complex; OMPC; Neisseria; AIDS; cyclic; cPND30.

KW Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein

FT complex"

FT Modified-site 2

FT /note= "epsilon-amino forms cyclic peptide with C-

FT terminal COOH group"

FT Modified-site 10

FT /note= "condenses with side chain NH2 of Lys(2) to give

FT cyclic peptide"

XX

PN EP468714-A.

XX 29-JAN-1992.

PD 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

PI WPI; 1992-034437/05.

DR HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

XX produce antibodies to prevent or treat HIV infection.

PS Claim 9; Page 56; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing

CC determinant (PND), or an immunologically equivalent peptide (PEP),

CC covalently coupled to an immunogenic protein or protein complex through

CC an anionic polysaccharide linker. Pref. the immunogenic protein is the

CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the

CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,

CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.

CC The present sequence (cPND30) is an example of a PND peptide component.

CC The conjugates are used for inducing HIV-neutralising antibodies or for

CC making vaccines to prevent contraction of HIV infection or disease. The

CC antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for

XX treating AIDS, or in diagnostic assays

SQ Sequence 10 AA;

Query Match 46.6%; Score 27; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7

Db 3 HIGPGRV 9

RESULT 43

AAW08545

ID AAW08545 standard; protein; 11 AA.

XX AAW08545;

AC 23-SEP-1997 (first entry)

DT C6 human sFv antibody C6.5 variable light chain (CDR3 mutant C6ML3-17.

DE Tumour; immune response; cytotoxin; carcinoma; breast cancer.

XX Homo sapiens.

OS Synthetic.

XX WO9700271-A1.

PN 03-JAN-1997.

PD 13-JUN-1996; 96WO-US010287.

XX 14-JUN-1995; 95US-0000238P.

PR 15-JUN-1995; 95US-0000250P.

XX (REGC) UNIV CALIFORNIA.

XX

PI Marks JD, Schier R;
 XX WPI; 1997-077488/07.
 DR
 XX New C6 human antibody binding specifically to c-erbB-2 - useful for
 PT treatment and diagnosis of tumours, with reduced risk of generating
 PT immune response.
 XX
 PS Claim 10; Page 93; 117pp; English.
 XX
 CC The present sequence represents a variable light chain CDR3 mutant C6ML3-
 CC 17 modified from the derived light chain variable region of the C6 human
 CC antibody C6.5. The mutant C6ML3-17 specifically binds to c-erbB-2. A
 CC chimeric molecule that binds specifically to tumour cells carrying c-erbB
 CC -2 consists of an effector compound attached to a C6 human antibody. If
 CC the effector compound is a cytotoxin the chimeric molecule can be used to
 CC inhibit growth of c-erbB-2 positive tumours (especially breast and other
 CC carcinomas). If the effector compound is a label the chimeric molecule
 CC can be used to detect such cells, including in vivo localisation. The
 CC antibody can also be used for diagnosis/localisation, in vivo or in
 CC vitro, especially by immunoassay. The nucleic acid encoding the antibody,
 CC and a nucleic acid encoding a single chain polypeptide with the binding
 CC specificity of the antibody and comprising the binding portions of
 CC variable regions of light and heavy chains of the antibody, joined by a
 CC linker, can be used to produce recombinant proteins by standard methods.
 CC Unlike known anti-c-erbB-2 antibodies, C6 antibodies are fully human, so
 CC should elicit little, if any, immunogenic response
 XX
 SQ Sequence 11 AA;
 Query Match 46.6%; Score 27; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPQWV 7
 Db :| |||
 5 YYRSGWV 11
 RESULT 44
 AAW08535
 ID AAW08535 standard; protein; 11 AA.
 XX
 AC AAW08535;
 XX
 DT 23-SEP-1997 (first entry)
 XX
 DE C6 human sFv antibody C6.5 variable light chain CDR3 mutant C6ML3-16.
 XX
 KW Tumour; immune response; cytotoxin; carcinoma; breast cancer.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9700271-A1.
 XX
 PD 03-JAN-1997.
 XX
 PF 13-JUN-1996; 96WO-US010287.
 XX
 PR 14-JUN-1995; 95US-0000238P.
 PR 15-JUN-1995; 95US-0000250P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Marks JD, Schier R;
 XX WPI; 1997-077488/07.
 DR
 XX New C6 human antibody binding specifically to c-erbB-2 - useful for
 PT treatment and diagnosis of tumours, with reduced risk of generating
 PT immune response.
 PT

PS Claim 10; Page 93; 117pp; English.
 XX
 CC The present sequence represents a variable light chain CDR3 mutant C6ML3-
 CC 16 modified from the derived light chain variable region of the C6 human
 CC antibody C6.5. The mutant C6ML3-16 specifically binds to c-erbB-2. A
 CC chimeric molecule that binds specifically to tumour cells carrying c-erbB
 CC -2 consists of an effector compound attached to a C6 human antibody. If
 CC the effector compound is a cytotoxin the chimeric molecule can be used to
 CC inhibit growth of c-erbB-2 positive tumours (especially breast and other
 CC carcinomas). If the effector compound is a label the chimeric molecule
 CC can be used to detect such cells, including in vivo localisation. The
 CC antibody can also be used for diagnosis/localisation, in vivo or in
 CC vitro, especially by immunoassay. The nucleic acid encoding the antibody,
 CC and a nucleic acid encoding a single chain polypeptide with the binding
 CC specificity of the antibody and comprising the binding portions of
 CC variable regions of light and heavy chains of the antibody, joined by a
 CC linker, can be used to produce recombinant proteins by standard methods.
 CC Unlike known anti-c-erbB-2 antibodies, C6 antibodies are fully human, so
 CC should elicit little, if any, immunogenic response
 XX
 SQ Sequence 11 AA;
 Query Match 46.6%; Score 27; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPQWV 7
 Db :| |||
 5 YYRSGWV 11
 RESULT 45
 ADC44682
 ID ADC44682 standard; peptide; 12 AA.
 XX
 AC ADC44682;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Endothelial cell binding peptide SEQ ID NO:411.
 XX
 KW endothelial cell binding protein; ECEP; anti-tumour; cytostatic;
 KW vasotrophic; antipsoriatic; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnerary; antitumor; antiinflammatory;
 KW antibacterial; gynaecological; angiogenesis.
 XX
 OS Synthetic.
 XX
 PN WO2003037172-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035258.
 XX
 PR 01-NOV-2001; 2001US-0334822P.
 XX
 PA (GPCB-) GPC BIOTECH INC.
 XX
 PI Gyuris J, Lamphere L, Morris AJ, Tsaioun K;
 XX WPI; 2003-482072/45.
 DR
 XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 XX
 PS Claim 3; SEQ ID NO 411; 126pp; English.
 XX
 CC The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECEP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotrophic, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnerary, antitumor,
 CC

CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC is useful for promoting, reducing the proliferation and/or migration of
CC endothelial cells, by treating the cells with an ECBP agonist, which is
CC preferably the peptide, to promote proliferation and/or migration of the
CC treated cells, and for reducing or promoting angiogenesis, by treating
CC the cells with an ECBP antagonist, which is preferably the peptide of the
CC invention. A peptide of the invention is also useful for manufacturing a
CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
CC a treated mammal. The medicament is useful for promoting or reducing
CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
CC of a viral particle. The present sequence represents an ECBP of the
CC invention.

XX

SQ Sequence 12 AA;

Query Match 46.6%; Score 27; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HYGPGWVS 8
Db 3 HQASGWT 10

Search completed: August 30, 2004, 10:49:37
Job time : 15.4088 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 14.8986 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITTVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	3	AAY69929 Human cyc
2	49	89.1	10	3	AAY69949 Human cyc
3	30	54.5	8	3	AAY69948 Human cyc
4	30	54.5	13	6	ABU11914 Human HGP
5	30	54.5	13	6	ABU11931 Human HGP
6	29	52.7	14	4	AAG98085 Human SNP
7	29	52.7	14	4	AAB29764 Equus sp.
8	27	49.1	13	2	AAW78212 Human sec
9	25.5	46.4	11	4	ABP18094 HIV B58 s
10	25	45.5	9	4	ABP21178 HIV A03 m
11	25	45.5	9	4	ABP13475 HIV A02 s
12	25	45.5	9	5	Aau94469 Human nov
13	25	45.5	9	5	Aau94677 Human nov
14	25	45.5	9	5	Aau94889 Human nov
15	25	45.5	10	4	ABP21186 HIV A03 m
16	25	45.5	10	4	ABP11874 HIV A01 s
17	25	45.5	10	4	ABP16363 HIV A24 s
18	25	45.5	10	5	ABP61558 Human KRP
19	25	45.5	10	5	AAM47755 p36 trypt
20	25	45.5	10	5	ABG98537 F protein
21	25	45.5	10	5	ABG98536 F protein
22	25	45.5	10	5	Aau95405 Human nov
23	25	45.5	10	5	Aau94768 Human nov
24	25	45.5	10	5	Aau94575 Human nov
25	25	45.5	10	5	Aau95402 Human nov

26	25	45.5	12	7	ADC44696 Endotheli
27	25	45.5	13	3	AAB38906 HIV-1 pep
28	25	45.5	13	3	AAB38842 HIV-1 pep
29	24	43.6	10	2	AAR79122 Algal lec
30	24	43.6	10	2	AAW09941 Peptide f
31	24	43.6	10	4	AAG86162 Saccharom
32	24	43.6	11	2	AAW21219 Farnesyl
33	24	43.6	11	4	AAM97289 Human pep
34	24	43.6	12	2	AAR52697 pASK46-pl
35	24	43.6	12	2	AAR52696 pASK46-pl
36	24	43.6	12	6	ABP99066 ErbB2 cel
37	24	43.6	12	6	ABU14354 C- or N-t
38	24	43.6	12	6	ABU14171 N-termina
39	24	43.6	12	6	ABU14170 N-termina
40	24	43.6	12	6	ABU14355 C- or N-t
41	24	43.6	12	6	ABU14172 N-termina
42	24	43.6	12	6	ABU14353 C- or N-t
43	24	43.6	12	6	ABU14173 N-termina
44	24	43.6	13	3	AAB38907 HIV-1 pep
45	24	43.6	13	3	AAB38843 HIV-1 pep

ALIGNMENTS

RESULT 1
AAY69929
ID AAY69929 standard; peptide; 10 AA.
XX
AC AAY69929;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #9.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFITTVKTAW 10
|||||

Db 1 FFITTVKTAW 10

RESULT 2

AAAY69949

ID AAY69949 standard; peptide; 10 AA.

XX

AC AAY69949;

XX

DT 11-APR-2000 (first entry)

XX

DE Human cyclophilin B peptide fragment #29.

XX

KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX

OS Homo sapiens.

XX

PN WO9967288-A1.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-JP003360.

XX

PR 25-JUN-1998; 98JP-00178449.

XX

PA (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

XX

PI Itoh K, Gomi S;

XX

DR WPI; 2000-116932/10.

XX

PT Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.

XX

PS Claim 4; Page 57; 64pp; Japanese.

XX

CC This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

XX

SQ Sequence 10 AA;

Query Match 89.1%; Score 49; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.031; Length 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFITTVKTAW 10

Db 1 FFITTVKTAW 9

RESULT 3

AAAY69948

ID AAY69948 standard; peptide; 8 AA.

XX

AC AAY69948;

XX

DT 11-APR-2000 (first entry)

XX

DE Human cyclophilin B peptide fragment #28.

XX

KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX

OS Homo sapiens.

XX

PN WO9967288-A1.

XX

PD 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-JP003360.

XX

PR 25-JUN-1998; 98JP-00178449.

XX

PA (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

XX

PI Itoh K, Gomi S;

XX

DR WPI; 2000-116932/10.

XX

PT Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.

XX

PS Claim 4; Page 56; 64pp; Japanese.

XX

CC This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

XX

SQ Sequence 8 AA;

Query Match 54.5%; Score 30; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFITTV 6

Db 3 FFITTV 8

RESULT 4

ABU11914

ID ABU11914 standard; peptide; 13 AA.

XX

AC ABU11914;

XX

DT 13-FEB-2003 (first entry)

XX

DE Human HGPBMY11 PKC phosphorylation site #1.

XX

KW Human; immungen; HGPBMY11; HGPBMY11v1; HGPBMY11v2; GPCR74; GPCR81;

KW G-protein coupled receptor; cardiovascular disease; arrhythmia;

KW myocardial infarction; congestive heart failure; cardiomyopathy;

KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;

KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;

KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;

KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;

KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.

XX

OS Homo sapiens.

XX

PN WO200286123-A2.

XX

PD 31-OCT-2002.

XX

PF 16-NOV-2001; 2001WO-US044019.

XX

PR 17-NOV-2000; 2000US-0249613P.

PR 21-DEC-2000; 2000US-0257611P.

PR 16-JUL-2001; 2001US-0305818P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;

XX

DR WPI; 2003-093137/08.

XX

PT New human G-protein coupled receptor HGPBMY11 polypeptide or polynucleotide, useful for preventing, treating or ameliorating e.g. myocardial infarction, angina, thrombosis, Alzheimer's disease, schizophrenia, AIDS, leukemia.

XX PS Disclosure; Page 48; 444pp; English.

XX CC The invention relates to an isolated polypeptide (designated HGPBMY11),

CC which has a G-protein coupled receptor (GPCR) activity (also known as

CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit

CC Number PTA-2766, its variants (HGPBMY11v1 and HGPBMY11v2), fragments,

CC domains, species homologues and proteins 95% similar to it. Also included

CC are: (1) the nucleic acids encoding the HGPBMY11 proteins (including

CC variants, fragments, complements and sequences 95% similar to the

CC HGPBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host

CC cells expressing HGPBMY11; (4) an anti-HGPBMY11 antibody; (5)

CC diagnosing a pathological condition or a susceptibility to a pathological

CC condition in a subject; (6) identifying a binding partner to the

CC HGPBMY11 polypeptide; (7) identifying an activity in a biological assay;

CC (8) a process for making polynucleotide sequences encoding a gene product

CC having altered GPCR activity; (9) a shuffled polynucleotide produced by

CC the method of (8); and (10) screening for candidate compounds capable of

CC binding to and/or modulating activity of a GPCR. The polypeptide or the

CC polynucleotide is useful for preventing, treating or ameliorating a

CC medical condition, particularly cardiovascular diseases or disorders,

CC e.g. myocardial infarction, congestive heart failure, arrhythmias,

CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,

CC thrombosis or hypertension). The HGPBMY11 polypeptide or polynucleotide

CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's

CC disease, Parkinson's disease, osteoporosis, obesity, human

CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,

CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,

CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other

CC diseases and disorders are listed in the specification). The present

CC sequence represents a protein motif or domain of an HGPBMY11 protein (or

CC variant) which may be used as an immugen

XX SQ Sequence 13 AA;

Query Match 54.5%; Score 30; DB 6; Length 13;

Best Local Similarity 37.5%; Pred. No. 1e+02;

Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10

Db 4 VTSIRSAW 11

RESULT 5

ABU11931

ID ABU11931 standard; peptide; 13 AA.

XX AC ABU11931;

XX DT 13-FEB-2003 (first entry)

XX DE Human HGPBMY11v1 PKC phosphorylation site #1.

XX KW Human; immugen; HGPBMY11; HGPBMY11v1; HGPBMY11v2; GPCR74; GPCR81;

KW G-protein coupled receptor; cardiovascular disease; arrhythmia;

KW myocardial infarction; congestive heart failure; cardiomyopathy;

KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;

KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;

KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;

KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;

KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.

XX OS Homo sapiens.

XX PN WO200286123-A2.

XX PD 31-OCT-2002.

XX PF 16-NOV-2001; 2001WO-US044019.

XX PR 17-NOV-2000; 2000US-0249613P.

PR 21-DEC-2000; 2000US-0257611P.

PR 16-JUL-2001; 2001US-0305818P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;

XX WPI; 2003-093137/08.

XX PT New human G-protein coupled receptor HGPBMY11 polypeptide or

PT polynucleotide, useful for preventing, treating or ameliorating e.g.

PT myocardial infarction, angina, thrombosis, Alzheimer's disease,

PT schizophrenia, AIDS, leukemia.

XX PS Disclosure; Page 76; 444pp; English.

XX CC The invention relates to an isolated polypeptide (designated HGPBMY11),

CC which has a G-protein coupled receptor (GPCR) activity (also known as

CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit

CC Number PTA-2766, its variants (HGPBMY11v1 and HGPBMY11v2), fragments,

CC domains, species homologues and proteins 95% similar to it. Also included

CC are: (1) the nucleic acids encoding the HGPBMY11 proteins (including

CC variants, fragments, complements and sequences 95% similar to the

CC HGPBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host

CC cells expressing HGPBMY11; (4) an anti-HGPBMY11 antibody; (5)

CC diagnosing a pathological condition or a susceptibility to a pathological

CC condition in a subject; (6) identifying a binding partner to the

CC HGPBMY11 polypeptide; (7) identifying an activity in a biological assay;

CC (8) a process for making polynucleotide sequences encoding a gene product

CC having altered GPCR activity; (9) a shuffled polynucleotide produced by

CC the method of (8); and (10) screening for candidate compounds capable of

CC binding to and/or modulating activity of a GPCR. The polypeptide or the

CC polynucleotide is useful for preventing, treating or ameliorating a

CC medical condition, particularly cardiovascular diseases or disorders,

CC e.g. myocardial infarction, congestive heart failure, arrhythmias,

CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,

CC thrombosis or hypertension). The HGPBMY11 polypeptide or polynucleotide

CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's

CC disease, Parkinson's disease, osteoporosis, obesity, human

CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,

CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,

CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other

CC diseases and disorders are listed in the specification). The present

CC sequence represents a protein motif or domain of an HGPBMY11 protein (or

CC variant) which may be used as an immugen

XX SQ Sequence 13 AA;

Query Match 54.5%; Score 30; DB 6; Length 13;

Best Local Similarity 37.5%; Pred. No. 1e+02;

Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10

Db 4 VTSIRSAW 11

RESULT 6

AAG98085

ID AAG98085 standard; peptide; 14 AA.

XX AC AAG98085;

XX DT 19-SEP-2001 (first entry)

XX DE Human SNP associated peptide SEQ ID NO. 727.

XX KW Human; single nucleotide polymorphism; SNP; angiotensin;

KW 4-hydroxybutyrate; dehydrogenase; protein therapy;

KW adenosine triphosphate-dependent RNA helicase;

KW major histocompatibility complex Class I histocompatibility antigen; MHC;

KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;

KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;

KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.

XX Homo sapiens.
OS WO200148245-A2.
PN 05-JUL-2001.
XX 27-DEC-2000; 2000WO-US035346.
XX 27-DEC-1999; 99US-00472688.
XX (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach M;
PI WPI; 2001-418297/44.
XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections.
XX Disclosure; Page 450; 484pp; English.
XX The invention relates to nucleic acids (AAH793386-AAH80036) encoding
CC polymorphic variants of proteins (AAG98010-AAG98238) related to
CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
CC histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
CC nervous system, an infection of pathogenic organisms. They may also be
CC used to alter phenotypic traits such as longevity, appearance, strength,
CC speed and endurance
XX Sequence 14 AA;
SQ
Query Match 52.7%; Score 29; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTVKTAW 10
Db 6 TSLKTSW 12
RESULT 7
AAB29764
ID AAB29764 standard; peptide; 14 AA.
XX AAB29764;
XX 06-AUG-2003 (revised)
DT 28-FEB-2001 (first entry)
XX Equus sp./gundi alpha globin.
DE Haemoglobin; rHb1.1; bacterial expression;
XX N-terminal methionine methylation signal; demethylation;
KW Escherichia coli; non-immunogenic; pharmaceutical composition; horse;
KW donkey; zebra; kulan; onager; gundi.

XX Equus caballus.
OS Equus asinus.
OS Equus zebra.
OS Equus hemionus.
OS Ctenodactylus gundi.
XX US6140071-A.
PN 31-OCT-2000.
XX 27-JAN-1994; 94US-00188374.
XX 27-JAN-1994; 94US-00188374.
PR (SOMA-) SOMATOGEN INC.
PA Aitken JF, Apostol IZ, Levine JD, Lippincott JA;
XX WPI; 2001-048957/06.
XX Decreasing methylation of an N-terminus protein, especially hemoglobin
PT having proline at amino acid position 4, useful for producing
PT demethylated proteins for treating diseases, by altering this amino acid
PT to a non-proline residue.
XX Disclosure; Col 5; 26pp; English.
XX The invention relates to a method of decreasing the amount of N-terminal
CC methionine methylation on a protein expressed in a bacterium. The
CC bacterial methyltransferase which directs N-terminal methionine
CC methylation recognises proteins which have a proline residue at position
CC 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
CC protein CheZ). The method comprises introducing mutations into the DNA
CC encoding the protein so that residue 4 is a non-proline residue, thereby
CC reducing the degree of N-terminal methylation when the protein is
CC expressed in a bacterium. The method is useful for decreasing methylation
CC of a protein, particularly a recombinantly produced protein. The
CC demethylated protein can be used in a pharmaceutical composition for the
CC treatment of a disease but with less likelihood of eliciting an
CC immunological response. These demethylated proteins may be used as
CC therapeutic agent for the treatment and/or amelioration of disease or
CC symptoms associated with a disease. The exemplifications describe the
CC expression of a recombinant human haemoglobin construct (rHb1.1) in
CC Escherichia coli, and its modification such that residue 4 of the di-
CC alpha chain of the recombinant haemoglobin is altered from proline to a
CC non-proline residue. The present sequence represents a peptide referred
CC to in the disclosure of the invention. (Updated on 06-AUG-2003 to correct
CC OS field.)
XX Sequence 14 AA;
SQ
Query Match 52.7%; Score 29; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 TTVKTAW 10
Db 8 TNVKAAW 14
RESULT 8
AAW78212
ID AAW78212 standard; protein; 13 AA.
XX AAW78212;
AC 13-APR-1999 (first entry)
XX Human secreted protein encoded by gene 9 clone HPFCY51.
DE Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW

KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FT Misc-difference 10
FT /label= unknown
FT Misc-difference 13
FT /label= unknown
XX
PN WO9856804-A1.
XX
PD 17-DEC-1998.
XX
PF 11-JUN-1998; 98WO-US012125.
XX

PR 13-JUN-1997; 97US-0049547P.
PR 13-JUN-1997; 97US-0049548P.
PR 13-JUN-1997; 97US-0049549P.
PR 13-JUN-1997; 97US-0049550P.
PR 13-JUN-1997; 97US-0049556P.
PR 13-JUN-1997; 97US-0049606P.
PR 13-JUN-1997; 97US-0049607P.
PR 13-JUN-1997; 97US-0049608P.
PR 13-JUN-1997; 97US-0049609P.
PR 13-JUN-1997; 97US-0049610P.
PR 13-JUN-1997; 97US-0049611P.
PR 13-JUN-1997; 97US-0050901P.
PR 13-JUN-1997; 97US-0052989P.
PR 08-JUL-1997; 97US-0051919P.
PR 18-AUG-1997; 97US-0055984P.
PR 12-SEP-1997; 97US-0058665P.
PR 12-SEP-1997; 97US-0058668P.
PR 12-SEP-1997; 97US-0058669P.
PR 12-SEP-1997; 97US-0058750P.
PR 12-SEP-1997; 97US-0058971P.
PR 12-SEP-1997; 97US-0058972P.
PR 12-SEP-1997; 97US-0058975P.
PR 02-OCT-1997; 97US-0060834P.
PR 02-OCT-1997; 97US-0060841P.
PR 02-OCT-1997; 97US-0060844P.
PR 02-OCT-1997; 97US-0060865P.
PR 02-OCT-1997; 97US-0061059P.
PR 02-OCT-1997; 97US-0061060P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;
PI Feng P;
XX

DR WPI; 1999-080881/07.
DR N-PSDB; AAX04397.

PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 11; Page 313; 380pp; English.
XX

CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAX04302) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 86 novel
CC genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino
CC acid sequences AAW78126-W78225) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,

CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 86 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAX04311 for described uses)
XX
SQ Sequence 13 AA;

Query Match 49.1%; Score 27; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVKT 8
Db 5 FFVTXLTL 12

RESULT 9

ABP18094
ID ABP18094 standard; peptide; 11 AA.
XX

AC ABP18094;
XX

DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX

DE HIV B58 super motif pol peptide #87.
XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX

OS Human immunodeficiency virus 1.
XX

PN WO200124810-A1.
XX

PD 12-APR-2001.
XX

PF 05-OCT-2000; 2000WO-US027766.
XX

PR 05-OCT-1999; 99US-00412863.
XX

PA (EPIM-) EPIMMUNE INC.
XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX

DR WPI; 2001-354887/37.
XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX

PS Claim 32; Page 239; 448pp; English.
XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 11 AA;
SQ Query Match 46.4%; Score 25.5; DB 4; Length 11;
Best Local Similarity 63.6%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 FFITTVKTA-W 10
| | | | |
Db 1 FTSTTVKAACW 11

RESULT 10
ABP211178
ID ABP211178 standard; peptide; 9 AA.
XX
AC ABP211178;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif pol peptide #173.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 303; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 9 AA;
SQ Query Match 45.5%; Score 25; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| | | | |
Db 1 FTSTTVKAA 9

RESULT 11
ABP13475
ID ABP13475 standard; peptide; 9 AA.
XX
AC ABP13475;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif pol peptide #390.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 144; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 9 AA;

Query Match 45.5%; Score 25; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| | | | |
Db 1 FTSTTVKAA 9

RESULT 12
AAU94469
ID AAU94469 standard; peptide; 9 AA.
XX AC AAU94469;
XX DT 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #202.
DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX OS Homo sapiens.
XX WO200214361-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025782.
XX PR 17-AUG-2000; 2000US-0226329P.
XX PA (AGEN-) AGENSYS INC.
PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
a subject, comprises determining the status of 83P2H3 gene products in a
tissue sample from the subject and comparing it to a normal sample.
PS Example 11; Page 179; 270pp; English.
XX The invention relates to monitoring 83P2H3 (a calcium transport protein
whose gene is located on chromosome 7q34) gene products in a biological
sample from a patient who has or is suspected of having cancer
(especially prostate cancer), comprises: (a) determining the status of
83P2H3 gene products expressed by cells in a tissue sample from an
individual and (b) comparing the status to the status of 83P2H3 gene
products in a normal sample. Also included are modulators of 83P2H3
function or status, generating antibodies/immune response against 83P2H3
(or related protein CaTrF2E11 whose gene is located on chromosome
12q24.1) using identified HLA (human leukocyte antigen) binding peptides
derived from the protein, delivering a cytotoxic agent to a cell
expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
recombinant protein comprising an antigen-binding region of the antibody, a
hybridoma that produces the recombinant protein, a single-chain
monoclonal antibody that comprises the variable domains of the heavy and
light chains of the anti-83P2H3 antibody, a vector comprising a
polynucleotide that encodes the monoclonal antibody and inducing an
immune response to a 83P2H3 protein, by providing a 83P2H3-related
protein that comprises a T cell or B cell epitope, and contacting the
epitope with an immune system T cell or B cell, respectively. The method
is useful for monitoring 83P2H3 gene products in a biological sample for
monitoring the presence of cancer in an individual. The modulator is
useful for inhibiting the growth of cancer cells that express 83P2H3, for
treating cancer and the vector is useful for treating a patient with a

cancer that expresses 83P2H3. The immunological methods are useful for
generating an immune response against 83P2H3, and for detecting the
presence of 83P2H3-related protein or polynucleotide in a biological
sample from a patient who has or is suspected of having cancer. The
antibody is useful in prostate cancer diagnosis, prognosis, imaging
methodologies and treatment, to detect and quantify 83P2H3 and mutant
83P2H3-related proteins, for purifying a 83P2H3-related protein, for
isolating 83P2H3 homologues/related molecules, and for generating anti-
idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
is an HLA binding peptide motif from 83P2H3 or its related protein
CaTrF2E11

SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
| | | | |
Db 3 FFFFTNIK 9

RESULT 13
AAU94677
ID AAU94677 standard; peptide; 9 AA.
XX AC AAU94677;
XX DT 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #310.
DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX OS Homo sapiens.
XX WO200214361-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US025782.
XX PR 17-AUG-2000; 2000US-0226329P.
XX PA (AGEN-) AGENSYS INC.
PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
a subject, comprises determining the status of 83P2H3 gene products in a
tissue sample from the subject and comparing it to a normal sample.
PS Example 11; Page 186; 270pp; English.
XX The invention relates to monitoring 83P2H3 (a calcium transport protein
whose gene is located on chromosome 7q34) gene products in a biological
sample from a patient who has or is suspected of having cancer
(especially prostate cancer), comprises: (a) determining the status of
83P2H3 gene products expressed by cells in a tissue sample from an
individual and (b) comparing the status to the status of 83P2H3 gene
products in a normal sample. Also included are modulators of 83P2H3
function or status, generating antibodies/immune response against 83P2H3
(or related protein CaTrF2E11 whose gene is located on chromosome
12q24.1) using identified HLA (human leukocyte antigen) binding peptides
derived from the protein, delivering a cytotoxic agent to a cell
expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
recombinant protein comprising an antigen-binding region of the antibody, a
hybridoma that produces the recombinant protein, a single-chain
monoclonal antibody that comprises the variable domains of the heavy and
light chains of the anti-83P2H3 antibody, a vector comprising a
polynucleotide that encodes the monoclonal antibody and inducing an
immune response to a 83P2H3 protein, by providing a 83P2H3-related
protein that comprises a T cell or B cell epitope, and contacting the
epitope with an immune system T cell or B cell, respectively. The method
is useful for monitoring 83P2H3 gene products in a biological sample for
monitoring the presence of cancer in an individual. The modulator is
useful for inhibiting the growth of cancer cells that express 83P2H3, for
treating cancer and the vector is useful for treating a patient with a

CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single- chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FFITTVK 7
Db 3 FFFTNIK 9
RESULT 14
AAU94889
ID AAU94889 standard; peptide; 9 AA.
XX
AC AAU94889;
XX
DT 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #422.
XX
DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
XX calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
KW
XX Homo sapiens.
OS
XX WO200214361-A2.
XX
PN 21-FEB-2002.
XX
PD 17-AUG-2001; 2001WO-US025782.
XX
PF 17-AUG-2000; 2000US-0226329P.
XX
PR (AGEN-) AGENSYS INC.
XX
PA Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
XX Levin E, Hubert RS, Ge W, Jakobovits A;
PI WPI; 2002-269179/31.
XX
DR Monitoring 83P2H3 gene products for monitoring the presence of cancer in
XX a subject, comprises determining the status of 83P2H3 gene products in a
PT tissue sample from the subject and comparing it to a normal sample.
PT
XX Example 11; Page 194; 270pp; English.
PS
XX The invention relates to monitoring 83P2H3 (a calcium transport protein

CC whose gene is located on chromosome 7q34) gene products in a biological
CC sample from a patient who has or is suspected of having cancer
CC (especially prostate cancer), comprises: (a) determining the status of
CC 83P2H3 gene products expressed by cells in a tissue sample from an
CC individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against 83P2H3
CC (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
CC derived from the protein, delivering a cytotoxic agent to a cell
CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
CC recombinant protein comprising an antigen-binding region of the antibody,
CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single- chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FFITTVK 7
Db 1 FFFTNIK 7
RESULT 15
ABP21186
ID ABP21186 standard; peptide; 10 AA.
XX
AC ABP21186;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif pol peptide #181.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
PT Claim 32; Page 303; 448pp; English.
PS The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10 AA;
Query Match 45.5%; Score 25; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FFITTVKTA 9
| | | | |
Db 2 FTSTTVKAA 10
RESULT 16
ABP11874
ID ABP11874 standard; peptide; 10 AA.
XX
AC ABP11874;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A01 super motif pol peptide #146.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX Claim 32; Page 112; 448pp; English.
PS The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10 AA;
Query Match 45.5%; Score 25; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FFITTVKTA 9
| | | | |
Db 1 FTSTTVKAA 9
RESULT 17
ABP16363
ID ABP16363 standard; peptide; 10 AA.
XX
AC ABP16363;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif pol peptide #543.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;

CC protein complex is a regulatory protein, which regulates the specificity
 CC of the channel forming protein for nucleic acid transport. Human
 CC cytosolic malate dehydrogenase (CMDH; AAM47750) was used as the second
 CC subunit protein in the invention. The protein complex is useful for
 CC reducing nucleic acid toxicity in kidney cells, and for facilitating the
 CC transport of nucleic acids into cells for a number of therapeutic
 CC applications. The present sequence is a p36 tryptic peptide, which was
 CC used in a sequence homology alignment with CMDH (given in Figure 3)
 XX
 SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITTVK 7
 Db 3 FITTVQ 8

RESULT 20
 ABG98537
 ID ABG98537 standard; peptide; 10 AA.
 XX
 AC ABG98537;

DT 13-JAN-2003 (first entry)
 XX
 DE F protein decapeptide #24.

KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;
 KW viral F protein; F protein mediated host cell virion fusion; virucide;
 KW F protein mediated host cell virion budding.

OS Respiratory syncytial virus.
 XX
 PN WO200242326-A1.

PD 30-MAY-2002.

PF 22-NOV-2001; 2001WO-AU001517.

PR 22-NOV-2000; 2000US-0252767P.

PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.

PI Mason AJ, Tucker SP, Young PR;

DR WPI; 2002-599372/64.

XX Facilitating production of a protein for analyzing, designing and/or
 PT modifying an agent that can interact with a viral F protein, comprises
 PT expressing a nucleic acid optimized for expression of the protein, using
 PT a eukaryotic cell.

PS Claim 42; Page 100; 367pp; English.

XX The invention relates to a method for facilitating production of a
 CC protein or its derivative from a negative sense single stranded RNA
 CC virus, by expressing a nucleic acid molecule encoding the protein in a
 CC host cell, where the nucleic acid is optimised for expression by a
 CC eukaryotic cell. The protein, especially F protein, is useful for
 CC analysing, designing and/or modifying an agent capable of interacting
 CC with a viral F protein or its derivative and modulating a functional
 CC activity associated with the protein, by contacting the protein with a
 CC putative agent and assessing the degree of interactive complementarity of
 CC the agent with the protein. An optimised nucleic acid or its derivative,
 CC equivalent, analogue or mimetic is useful for interacting with a viral F
 CC protein and modulating a functional activity associated with the viral
 CC protein, for use in the manufacture of a medicament utilised in the
 CC therapeutic and/or prophylactic treatment of conditions characterised by
 CC infection with a negative sense single stranded RNA virus, and for
 CC modulating a functional activity associated with a viral F protein in a

CC subject, preferably a mammal, especially a human, where the functional
 CC activity is F protein mediated host cell virion fusion and/or virion
 CC budding and the modulating is down regulation. Sequences ABG98514-
 CC ABG99058 represent F protein decapeptides of the invention
 XX
 SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 22.2%; Pred. No. 6.1e+02;
 Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
 Db 1 YLSALRTGW 9

RESULT 21
 ABG98536
 ID ABG98536 standard; peptide; 10 AA.
 XX
 AC ABG98536;

DT 13-JAN-2003 (first entry)
 XX
 DE F protein decapeptide #23.

KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;
 KW viral F protein; F protein mediated host cell virion fusion; virucide;
 KW F protein mediated host cell virion budding.

OS Respiratory syncytial virus.
 XX
 PN WO200242326-A1.

PD 30-MAY-2002.

PF 22-NOV-2001; 2001WO-AU001517.

PR 22-NOV-2000; 2000US-0252767P.

PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.

PI Mason AJ, Tucker SP, Young PR;

DR WPI; 2002-599372/64.

XX Facilitating production of a protein for analyzing, designing and/or
 PT modifying an agent that can interact with a viral F protein, comprises
 PT expressing a nucleic acid optimized for expression of the protein, using
 PT a eukaryotic cell.

PS Claim 42; Page 100; 367pp; English.

XX The invention relates to a method for facilitating production of a
 CC protein or its derivative from a negative sense single stranded RNA
 CC virus, by expressing a nucleic acid molecule encoding the protein in a
 CC host cell, where the nucleic acid is optimised for expression by a
 CC eukaryotic cell. The protein, especially F protein, is useful for
 CC analysing, designing and/or modifying an agent capable of interacting
 CC with a viral F protein or its derivative and modulating a functional
 CC activity associated with the protein, by contacting the protein with a
 CC putative agent and assessing the degree of interactive complementarity of
 CC the agent with the protein. An optimised nucleic acid or its derivative,
 CC equivalent, analogue or mimetic is useful for interacting with a viral F
 CC protein and modulating a functional activity associated with the viral
 CC protein, for use in the manufacture of a medicament utilised in the
 CC therapeutic and/or prophylactic treatment of conditions characterised by
 CC infection with a negative sense single stranded RNA virus, and for
 CC modulating a functional activity associated with a viral F protein in a
 CC subject, preferably a mammal, especially a human, where the functional
 CC activity is F protein mediated host cell virion fusion and/or virion
 CC budding and the modulating is down regulation. Sequences ABG98514-
 CC ABG99058 represent F protein decapeptides of the invention

XX SQ Sequence 10 AA; Query Match 45.5%; Score 25; DB 5; Length 10; Best Local Similarity 22.2%; Pred. No. 6.1e+02; Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10 ::::|:| Db 2 YLSALRTGW 10

RESULT 22 AAU95405 ID AAU95405 standard; peptide; 10 AA. XX AC AAU95405; XX DT 02-JUL-2002 (first entry) XX DE Human novel protein CaTrF2E11 HLA binding peptide #672. XX KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11; KW calcium transport protein; cancer; prostate cancer; cytostatic; KW chromosome 7q34; chromosome 12q24.1; T cell; B cell. XX OS Homo sapiens. XX PN WO200214361-A2. XX PD 21-FEB-2002. XX PF 17-AUG-2001; 2001WO-US025782. XX PR 17-AUG-2000; 2000US-0226329P. XX PA (AGEN-) AGENSYS INC. XX PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH; PI Levin E, Hubert RS, Ge W, Jakobovits A; XX DR WPI; 2002-269179/31. XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample. XX PS Example 11; Page 197; 270pp; English. XX CC The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological sample from a patient who has or is suspected of having cancer (especially prostate cancer), comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 function or status, generating antibodies/immune response against 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome 12q24.1) using identified HLA (human leukocyte antigen) binding peptides derived from the protein, delivering a cytotoxic agent to a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a recombinant protein comprising an antigen-binding region of the antibody, a non-human transgenic animal that produces the recombinant protein, a hybridoma that produces the recombinant protein, a single-chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the anti-83P2H3 antibody, a vector comprising a polynucleotide that encodes the monoclonal antibody and inducing an immune response to a 83P2H3 protein, by providing a 83P2H3-related protein that comprises a T cell or B cell epitope, and contacting the epitope with an immune system T cell or B cell, respectively. The method is useful for monitoring 83P2H3 gene products in a biological sample for monitoring the presence of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC treating cancer and the vector is useful for treating a patient with a cancer that expresses 83P2H3. The immunological methods are useful for generating an immune response against 83P2H3, and for detecting the presence of 83P2H3-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The antibody is useful in prostate cancer diagnosis, prognosis, imaging methods and treatment, to detect and quantify 83P2H3 and mutant 83P2H3-related proteins, for purifying a 83P2H3-related protein, for isolating 83P2H3 homologues/related molecules, and for generating anti-idiotypic antibodies that mimic the 83P2H3 protein. The present sequence is an HLA binding peptide motif from 83P2H3 or its related protein CaTrF2E11

XX SQ Sequence 10 AA; Query Match 45.5%; Score 25; DB 5; Length 10; Best Local Similarity 57.1%; Pred. No. 6.1e+02; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7 :|:|:| Db 1 FFFTNIK 7

RESULT 23 AAU94768 ID AAU94768 standard; peptide; 10 AA. XX AC AAU94768; XX DT 02-JUL-2002 (first entry) XX DE Human novel protein CaTrF2E11 HLA binding peptide #351. XX KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11; KW calcium transport protein; cancer; prostate cancer; cytostatic; KW chromosome 7q34; chromosome 12q24.1; T cell; B cell. XX OS Homo sapiens. XX PN WO200214361-A2. XX PD 21-FEB-2002. XX PF 17-AUG-2001; 2001WO-US025782. XX PR 17-AUG-2000; 2000US-0226329P. XX PA (AGEN-) AGENSYS INC. XX PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH; PI Levin E, Hubert RS, Ge W, Jakobovits A; XX DR WPI; 2002-269179/31. XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample. XX PS Example 11; Page 189; 270pp; English. XX CC The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological sample from a patient who has or is suspected of having cancer (especially prostate cancer), comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 function or status, generating antibodies/immune response against 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome 12q24.1) using identified HLA (human leukocyte antigen) binding peptides derived from the protein, delivering a cytotoxic agent to a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a

CC recombinant protein comprising an antigen-binding region of the antibody,
CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single-chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11

XX
SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 4 FFTNIK 10

RESULT 24

AAU94575
ID AAU94575 standard; peptide; 10 AA.

XX
AC AAU94575;

XX
DT 02-JUL-2002 (first entry)

XX Human novel protein CaTrF2E11 HLA binding peptide #258.

DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
XX calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

OS WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US025782.

XX 17-AUG-2000; 2000US-0226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;

XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
PT a subject, comprises determining the status of 83P2H3 gene products in a
PT tissue sample from the subject and comparing it to a normal sample.

XX Example 11; Page 182; 270pp; English.

XX

CC The invention relates to monitoring 83P2H3 (a calcium transport protein
CC whose gene is located on chromosome 7q34) gene products in a biological
CC sample from a patient who has or is suspected of having cancer
CC (especially prostate cancer), comprises: (a) determining the status of
CC 83P2H3 gene products expressed by cells in a tissue sample from an
CC individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against 83P2H3
CC (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
CC derived from the protein, delivering a cytotoxic agent to a cell
CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
CC recombinant protein comprising an antigen-binding region of the antibody,
CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single-chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11

XX
SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 4 FFTNIK 10

RESULT 25

AAU95402

ID AAU95402 standard; peptide; 10 AA.

XX AAU95402;

XX 02-JUL-2002 (first entry)

XX Human novel protein CaTrF2E11 HLA binding peptide #669.

XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US025782.

XX 17-AUG-2000; 2000US-0226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
DR
XX
PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in
PT a subject, comprises determining the status of 83P2H3 gene products in a
PT tissue sample from the subject and comparing it to a normal sample.
XX
PS Example 11; Page 197; 270pp; English.
XX
CC The invention relates to monitoring 83P2H3 (a calcium transport protein
CC whose gene is located on chromosome 7q34) gene products in a biological
CC sample from a patient who has or is suspected of having cancer
CC (especially prostate cancer), comprises: (a) determining the status of
CC 83P2H3 gene products expressed by cells in a tissue sample from an
CC individual and (b) comparing the status to the status of 83P2H3 gene
CC products in a normal sample. Also included are modulators of 83P2H3
CC function or status, generating antibodies/immune response against 83P2H3
CC (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
CC derived from the protein, delivering a cytotoxic agent to a cell
CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
CC recombinant protein comprising an antigen-binding region of the antibody,
CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single-chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83P2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83P2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83P2H3. The immunological methods are useful for
CC generating an immune response against 83P2H3, and for detecting the
CC presence of 83P2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
CC isolating 83P2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83P2H3 or its related protein
CC CaTrF2E11
XX
SQ Sequence 10 AA;
Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FFITTVK 7
Db ||| :|
2 FFFTNIX 8
RESULT 26
ADC44696
ID ADC44696 standard; peptide; 12 AA.
XX AC ADC44696;
XX
DT 18-DEC-2003 (first entry)
XX
DE Endothelial cell binding peptide SEQ ID NO:425.
XX
KW endothelial cell binding protein; ECBP; anti-tumour; cytostatic;
KW vasotrophic; antipsoriatic; dermatological; ophthalmological;
KW antidiabetic; antiarthritic; vulnery; antiulcer; antiinflammatory;

KW antibacterial; gynaecological; angiogenesis.
XX
OS Synthetic.
XX
PN WO2003037172-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US0352558.
XX
PR 01-NOV-2001; 2001US-0334822P.
XX
PA (GPCB-) GPC BIOTECH INC.
XX
PI Gyuris J, Lamphere L, Morris AJ, Tsaoun K;
XX WPI; 2003-482072/45.
DR
XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
PT proliferation and/or migration of endothelial cells, and for modulating
PT angiogenesis, has endothelial cell binding protein sequences.
XX
PS Claim 3; SEQ ID NO 425; 126pp; English.
XX
CC The invention relates to a novel isolated, synthetic or recombinant
CC peptide or polypeptide which includes one or more endothelial cell
CC binding protein (ECBP) sequences. A peptide of the invention has anti-
CC tumour, cytostatic, vasotrophic, antipsoriatic, dermatological,
CC ophthalmological, antidiabetic, antiarthritic, vulnery, antiulcer,
CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC is useful for promoting, reducing the proliferation and/or migration of
CC endothelial cells, by treating the cells with an ECBP agonist, which is
CC preferably the peptide, to promote proliferation and/or migration of the
CC treated cells, and for reducing or promoting angiogenesis, by treating
CC the cells with an ECBP antagonist, which is preferably the peptide of the
CC invention. A peptide of the invention is also useful for manufacturing a
CC medicament for promoting angiogenesis, by admixing an ECBP agonist or
CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
CC a treated mammal. The medicament is useful for promoting or reducing
CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
CC of a viral particle. The present sequence represents an ECBP of the
CC invention.
XX
SQ Sequence 12 AA;
Query Match 45.5%; Score 25; DB 7; Length 12;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 TVKTAW 10
Db ||| |
1 TVKAGW 6
RESULT 27
AAB38906
ID AAB38906 standard; peptide; 13 AA.
XX AC AAB38906;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #259.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX
OS Human immunodeficiency virus.
XX
PN WO200058438-A2.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.

XX 29-MAR-1999; 99US-0126938P.
XX (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
PI WPI; 2000-656164/63.
XX Synthetic peptides useful for preventing and treating HIV infection in
PT mammals, comprising a conformationally constrained portion and a portion
PT with continuous stretch of amino acids of predicted secondary structure.
XX Disclosure; Page 26; 69pp; English.
XX The present invention relates to peptides (AAB38648-B38970) comprising a
CC first conformationally constrained portion with a cross-linked group of a
CC HIV envelope protein that induces neutralising antibodies, and a second
CC portion comprising a continuous stretch of at least 5 amino acids having
CC a predicted secondary structure. The present sequence is one such
CC peptide. The peptides of the present invention are useful as a vaccine
CC for prophylactic or therapeutic treatment of a mammal for HIV infection
XX Sequence 13 AA;
SQ

Query Match 45.5%; Score 25; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 4 TTVK--TAW 10
Db 3 TTVKWNWSW 11

RESULT 28
AAB38842
ID AAB38842 standard; peptide; 13 AA.
XX AAB38842;
AC
XX 02-FEB-2001 (first entry)
DT
XX HIV-1 peptide epitope #195.
DE
XX Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX Human immunodeficiency virus.
XX WO200058438-A2.
PN
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000WO-US008232.
XX
XX 29-MAR-1999; 99US-0126938P.
XX (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
PI WPI; 2000-656164/63.
XX Synthetic peptides useful for preventing and treating HIV infection in
PT mammals, comprising a conformationally constrained portion and a portion
PT with continuous stretch of amino acids of predicted secondary structure.
XX Disclosure; Page 24; 69pp; English.

XX The present invention relates to peptides (AAB38648-B38970) comprising a
CC first conformationally constrained portion with a cross-linked group of a
CC HIV envelope protein that induces neutralising antibodies, and a second
CC portion comprising a continuous stretch of at least 5 amino acids having
CC a predicted secondary structure. The present sequence is one such
CC peptide. The peptides of the present invention are useful as a vaccine
CC for prophylactic or therapeutic treatment of a mammal for HIV infection
XX Sequence 13 AA;
SQ

Query Match 45.5%; Score 25; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 4 TTVK--TAW 10
Db 3 TTVKWNWSW 11

RESULT 29
AAR79122
ID AAR79122 standard; peptide; 10 AA.
XX AAR79122;
AC
XX 27-AUG-2003 (revised)
DT 21-FEB-1996 (first entry)
XX Algal lectin N-terminal with unique sugar-chain binding specificity.
DE
XX Algae; lectin; sugar; carbohydrate; specificity; diagnosis; therapy;
KW cancer; immunomodulator; transplant rejection; autoimmune disease.
XX Eucheuma sp.
OS
XX WO9518149-A1.
PN
XX 06-JUL-1995.
PD
XX 19-DEC-1994; 94WO-JP002140.
PF
XX 24-DEC-1993; 93JP-00328218.
PR (MARI-) MARINE GREENS LAB CO LTD.
XX Kawakubo A, Makino H, Ninomiya M, Bitou N;
PI WPI; 1995-246334/32.
DR
XX Algal lectin with unique sugar-chain binding specificity - deriv.from
PT Eucheuma or Kappaphycus species, is useful for diagnosis and therapy of
PT cancer and immune disorders.
XX Claim 1; Page 21; 38pp; Japanese.
PS
XX AAR79121 and AAR79122 are possible N-terminal peptides from a new algal
CC lectin which are derived from the Eucheuma species of alga. More
CC specifically the lectin is derived from either E.serra, E.cottonii,
CC E.gelatiniae or E.amakusaensis. The N-terminal peptides obey the general
CC formula G-R-Y-T-V-X-N-Q-W-G where X= Q or K. The lectins have a unique
CC ability to bind specifically to certain sugar-chains, and bind
CC specifically to fetuin, asialofetuin, thyroglobulin and yeast mannan. The
CC lectin may be used in a variety of ways; as an immunomodulator, as a
CC diagnostic and test reagent, as a specific adsorbent for separation and
CC analysis of sugars, as an organ transplant rejection inhibitor, as an
CC anticancer agent, for the treatment of autoimmune disease and as a
CC lymphocyte growth factor. (Updated on 27-AUG-2003 to correct OS field.)
XX Sequence 10 AA;
SQ

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
||| |
Db 4 TVKNQW 9

RESULT 30
AAW09941
ID AAW09941 standard; protein; 10 AA.
XX AC AAW09941;
XX DT 13-MAR-1998 (first entry)
XX DE Peptide from clone 11 from cell intrusion experiment.
XX KW Fusion protein; surface; bacterial cell; peptide library; aggregate;
KW screening; diagnosis; treatment; autoimmune disease; cancer.
XX OS Synthetic.
XX PN WO9706264-A1.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-JP002196.
XX PR 04-AUG-1995; 95JP-00199745.
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Shimbara N, Saya H;
XX WPI; 1997-154269/14.
DR N-PSDB; AAT66417.
XX Bacterial peptide library expressing cell invasive protein on the cell
PT surface - bonded to a random target protein which is thus introduced to
PT target cells.
XX Disclosure; Page 45; 86pp; Japanese.

Escherichia coli was introduced into VA13 to obtain a cell intrusion E.
coli. This was carried out using ESPEL. 22 clones were selected from this
and plasmid extracted. DNA sequencing was carried out by Taq cycle
sequencing. The invention concerns a fusion protein which presents at the
surface of bacterial cells transformed with DNA coding for the fusion
protein. Bacterium exhibiting the fused protein on its surface are used
to produce a bacterial peptide library which is an aggregate of such
bacteria. The bacterial peptide library is useful in identification of
target proteins having a desired biochemical activity in target cells,
for diagnosis or treatment of diseases such as autoimmune diseases and
cancer. The bacterial library readily reproduces and is relatively
stable, without significant change or denaturation during preservation

Sequence 10 AA;

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 TVKTAW 10
|:| |
Db 1 TMRRTW 6

RESULT 31
AAG86162
ID AAG86162 standard; peptide; 10 AA.
XX AC AAG86162;
XX

DT 11-SEP-2001 (first entry)
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 1111.
DE
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX WO200142276-A1.
PN 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004773.
PF 13-DEC-1999; 99GB-00029471.
PR (PROT-) PROTEOM LTD.
XX Roberts GW, Heal JR;
XX WPI; 2001-367863/38.
DR Identifying complementary peptides by analysis of protein and nucleotide
XX sequence databases, useful in drug design.
XX Example 3; Page 183; 488pp; English.
XX The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae
XX Sequence 10 AA;

Query Match 43.6%; Score 24; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
|| |
Db 2 VKAAW 6

RESULT 32
AAW21219
ID AAW21219 standard; peptide; 11 AA.
XX AC AAW21219;
XX DT 29-JUL-1997 (first entry)
XX Farnesyl synthetase derived signal oligopeptide #19.
DE
XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX Homo sapiens.
XX WO9519568-A1.
PN

XX 20-JUL-1995.
PD 12-JAN-1995; 95WO-US000575.
PF 14-JAN-1994; 94US-00182248.
XX (RATH/) RATH M.
PA Rath M;
XX WPI; 1995-263953/34.
PI Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).
XX Claim 5; Page 26; 88pp; English.
PS The sequences given in AAW21201-560 represent hydrophilic signal oligo-
XX peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX Sequence 11 AA;
SQ Query Match 43.6%; Score 24; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 FITTVKT 8
Db |||||
5 FIVTFKT 11
RESULT 33
AAM97289
ID AAM97289 standard; peptide; 11 AA.
XX AC AAM97289;
XX DT 24-JAN-2002 (first entry)
XX DE Human peptide #564 encoded by a SNP oligonucleotide.
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX OS Homo sapiens.
XX PN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
PI WPI; 2001-465210/50.
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX Disclosure; Page 3791; 4143pp; English.
PS The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX Sequence 11 AA;
SQ Query Match 43.6%; Score 24; DB 4; Length 11;
Best Local Similarity 37.5%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 ITTVKTAW 10
Db :||| : :
3 VTTYQSLW 10
RESULT 34
AAR52697
ID AAR52697 standard; protein; 12 AA.
XX AC AAR52697;
XX DT 10-JAN-1995 (first entry)
XX DE pASK46-pl1XL encoded C-terminal streptavidin-binding sequence.
XX KW Streptavidin binding peptide; fusion protein; immunoglobulin; Ig;
KW light chain variable region; affinity chromatography; purification;
KW peptide tag.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 5. .12
FT /note= "streptavidin-binding octapeptide fused to C-
FT terminus of VL chain"
XX GB2272698-A.
XX PN 25-MAY-1994.
XX PD 01-NOV-1993; 93GB-00022501.
XX PF 03-NOV-1992; 92DE-04237113.
XX PR

PA (BIOA-) INST BIOANALYTIK GEMEINNUTZIGE GMBH.
XX
XX Skerra A, Schmidt T;
XX
DR WPI; 1994-153484/19.
DR N-PSDB; AAQ62672.
XX
PT New fusion peptide(s) - have easily controlled binding properties and are
PT capable of binding to streptavidin.
XX
XX Disclosure; Page 11; 53pp; English.
XX
CC Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv
CC fragment in E.coli) were produced which encode 4 different peptides at
CC the C-terminus of VH and 2 peptides at the C-terminus of VL of the D1.3Fv
CC fragment. The peptides fused to the C-terminus are all examples of
CC streptavidin-binding peptides corresponding to a generic formula (see
CC AAR52698). The peptides do not interfere with the protein function but
CC facilitate purification by conferring streptavidin-binding properties on
CC the fusion protein
XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db :|:|
1 IKSAW 5

RESULT 35
AAR52696
ID AAR52696 standard; protein; 12 AA.
XX
AC AAR52696;
XX
DT 10-JAN-1995 (first entry)
XX
DE pASK46-p111L encoded C-terminal streptavidin-binding sequence.
XX
KW Streptavidin binding peptide; fusion protein; immunoglobulin; Ig;
KW light chain variable region; affinity chromatography; purification;
KW peptide tag.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 5..12
FT /note= "streptavidin-binding octapeptide fused to C-terminus of VL chain"
XX
PN GB2272698-A.
XX
PD 25-MAY-1994.
XX
PF 01-NOV-1993; 93GB-00022501.
XX
PR 03-NOV-1992; 92DE-04237113.
XX
PA (BIOA-) INST BIOANALYTIK GEMEINNUTZIGE GMBH.
XX
PI Skerra A, Schmidt T;
XX
XX WPI; 1994-153484/19.
DR N-PSDB; AAQ62671.
XX
PT New fusion peptide(s) - have easily controlled binding properties and are
PT capable of binding to streptavidin.
XX
PS Disclosure; Page 11; 53pp; English.
XX

CC Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv
CC fragment in E.coli) were produced which encode 4 different peptides at
CC the C-terminus of VH and 2 peptides at the C-terminus of VL of the D1.3Fv
CC fragment. The peptides fused to the C-terminus are all examples of
CC streptavidin-binding peptides corresponding to a generic formula (see
CC AAR52698). The peptides do not interfere with the protein function but
CC facilitate purification by conferring streptavidin-binding properties on
CC the fusion protein
XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db :|:|
1 IKSAW 5

RESULT 36
ABP99066
ID ABP99066 standard; peptide; 12 AA.
XX
AC ABP99066;
XX
DT 18-MAR-2003 (first entry)
XX
DE ErbB2 cell overexpression EOPI-98 peptide SEQ ID NO:103.
XX
KW ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
KW EOPI; EOF; ErbB2 overexpression feature; cytostatic; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200290991-A2.
XX
PD 14-NOV-2002.
XX
PF 02-MAY-2002; 2002WO-GB002047.
XX
PR 03-MAY-2001; 2001GB-00010886.
PR 23-NOV-2001; 2001GB-00028183.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Page MJ;
XX
DR WPI; 2003-103531/09.
XX
PT Diagnosing and treating ErbB2-related cancer, comprises generating ErbB2
PT Overexpression Features (EOFs) from test samples from a subject by
PT electrophoresis, and comparing the EOFs in the sample with a
PT predetermined reference range.
XX
PS Claim 3; Page 20; 106pp; English.
XX
CC The present invention describes a method for screening or diagnosing
CC ErbB2-related cancer. The method comprises generating ErbB2
CC overexpression features (EOFs) from test samples of body fluid from the
CC subject by electrophoresis, and comparing the EOFs in the test sample
CC with that from normal subjects or with an expression reference feature
CC (ERF) in the test sample. Also described: (1) an antibody capable of
CC immunospecific binding to an ErbB2 overexpression protein isoform (EOPI);
CC (2) pharmaceutical compositions comprising an EOPI, a nucleic acid
CC encoding an EOPI, an amount of the above antibody or its fragment, and a
CC carrier; (3) a kit comprising one or more antibodies and/or EOPIs cited
CC above, other reagents and instructions for use; (4) methods of treating
CC or preventing ErbB2-related cancer; (5) methods of screening for or
CC identifying agents that interact with or modulate the expression of
CC activity of, one or more EOPIs, EOPI fragment, EOPI-related polypeptides,
CC or EOPI-fusion proteins; (6) a method for modulating the activity of one

CC or more of the ErbB2 EOPIS, comprising administering to a subject an
CC agent identified by the method of (5); and (7) a method for identifying
CC targets for therapeutic modulation of ErbB2-related cancer. EOPIS have
CC cytostatic activity and can be used in vaccines and gene therapy. The
CC method is useful in screening, diagnosing, preventing or treating ErbB2-
CC related cancer, determining the stage or severity of ErbB2-related
CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
CC monitoring the effect of therapy administered to a subject with ErbB2-
CC related cancer, and for drug screening or drug development. The kit is
CC useful in carrying out the above methods. ABP98940 to ABP99206 represent
CC specifically claimed EOPIS from the present invention
XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVKT 8
| : ||| |
Db 4 FTLTTVDT 11

RESULT 37
ABU14354
ID ABU14354 standard; peptide; 12 AA.
XX
AC ABU14354;
XX
DT 12-MAR-2003 (first entry)
XX
DE C- or N-terminal cysteine containing hFSH peptide #100.
XX
KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; hFSH;
KW human follicle-stimulating hormone.
XX
OS Homo sapiens.
XX
PN WO200266984-A2.
XX
PD 29-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-NL0000097.
XX
PR 16-FEB-2001; 2001EP-00200551.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Puijk WC, Van Dijk E, Slootstra JW;
XX
DR WPI; 2003-103161/09.
XX
PT Novel support used for micro-arrays and its use in detection of (bio)
PT molecules.
XX
PS Example 3; Fig 6C; 4lpp; English.
XX
CC The present invention relates to a method for the detection of
CC biomolecules in pixel arrays and the supports used for the micro-arrays.
CC The novel supports for the micro-arrays are suitable for determining the
CC binding of a first member molecule within a library of spots of tentative
CC first member binding molecules with a second member binding molecule. The
CC support is provided with a support surface where surface patches are
CC interspersed with surface areas that are materially distinct from the
CC patches. The support and method of the invention are useful for
CC identifying or obtaining a synthetic molecule comprising a binding site,
CC or a binding molecule capable of binding to a binding site. The molecule
CC is useful for interfering with, or effecting binding to a binding
CC molecule. The novel support for a micro-array and the method provide high
CC density arraying (testing many binding events in one go) and enzyme-
CC linked-assays (very sensitive) allowing the detection of more binding

CC pairs more rapidly. ABU14255-ABU14437 represent human follicle-
CC stimulating hormone (hFSH) derived peptides containing a C- or N-terminal
CC cysteine. These peptides are used in the method of the present invention
XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : | |
Db 3 FCISINTTW 11

RESULT 38
ABU14171
ID ABU14171 standard; peptide; 12 AA.
XX
AC ABU14171;
XX
DT 28-FEB-2003 (first entry)
XX
DE N-terminal bromoacetamide containing hFSH peptide #98.
XX
KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW human follicle-stimulating hormone; hFSH.
XX
OS Homo sapiens.
XX
PN WO200266984-A2.
XX
PD 29-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-NL0000097.
XX
PR 16-FEB-2001; 2001EP-00200551.
XX
PA (PEPS-) PEPSCAN SYSTEMS BV.
XX
PI Puijk WC, Van Dijk E, Slootstra JW;
XX
DR WPI; 2003-103161/09.
XX
PT Novel support used for micro-arrays and its use in detection of (bio)
PT molecules.
XX
PS Example 3; Fig 6B; 4lpp; English.
XX
CC The present invention relates to a method for the detection of
CC biomolecules in pixel arrays and the supports used for the micro-arrays.
CC The novel supports for the micro-arrays are suitable for determining the
CC binding of a first member molecule within a library of spots of tentative
CC first member binding molecules with a second member binding molecule. The
CC support is provided with a support surface where surface patches are
CC interspersed with surface areas that are materially distinct from the
CC patches. The support and method of the invention are useful for
CC identifying or obtaining a synthetic molecule comprising a binding site,
CC or a binding molecule capable of binding to a binding site. The molecule
CC is useful for interfering with, or effecting binding to a binding
CC molecule. The novel support for a micro-array and the method provide high
CC density arraying (testing many binding events in one go) and enzyme-
CC linked-assays (very sensitive) allowing the detection of more binding
CC pairs more rapidly. ABU14074-ABU14254 represent human follicle-
CC stimulating hormone (hFSH) derived peptides containing an N-terminal
CC bromoacetamide group. These peptides are used in the method of the
XX present invention
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 3 FCISINTTW 11

RESULT 39

ABU14170
ID ABU14170 standard; peptide; 12 AA.

XX
AC ABU14170;

XX
DT 28-FEB-2003 (first entry)

XX
DE N-terminal bromoacetamide containing hFSH peptide #97.

XX
KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW human follicle-stimulating hormone; hFSH.

XX
OS Homo sapiens.

XX
PN WO200266984-A2.

XX
PD 29-AUG-2002.

XX
PF 15-FEB-2002; 2002WO-NL000097.

XX
PR 16-FEB-2001; 2001EP-00200551.

XX
PA (PEPS-) PEPSCAN SYSTEMS BV.

XX
PI Puijk WC, Van Dijk E, Slootstra JW;

XX
DR WPI; 2003-103161/09.

XX
PT Novel support used for micro-arrays and its use in detection of (bio)
PT molecules.

XX
PS Example 3; Fig 6B; 41pp; English.

XX
CC The present invention relates to a method for the detection of
CC biomolecules in pixel arrays and the supports used for the micro-arrays.
CC The novel supports for the micro-arrays are suitable for determining the
CC binding of a first member molecule within a library of spots of tentative
CC first member binding molecules with a second member binding molecule. The
CC support is provided with a support surface where surface patches are
CC interspersed with surface areas that are materially distinct from the
CC patches. The support and method of the invention are useful for
CC identifying or obtaining a synthetic molecule comprising a binding site,
CC or a binding molecule capable of binding to a binding site. The molecule
CC is useful for interfering with, or effecting binding to a binding
CC molecule. The novel support for a micro-array and the method provide high
CC density arraying (testing many binding events in one go) and enzyme-
CC linked-assays (very sensitive) allowing the detection of more binding
CC pairs more rapidly. ABU14074-ABU14254 represent human follicle-
CC stimulating hormone (hFSH) derived peptides containing an N-terminal
CC bromoacetamide group. These peptides are used in the method of the
CC present invention

XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 4 FCISINTTW 12

RESULT 40
ABU14355
ID ABU14355 standard; peptide; 12 AA.

XX
AC ABU14355;

XX
DT 12-MAR-2003 (first entry)

XX
DE C- or N-terminal cysteine containing hFSH peptide #101.

XX
KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; hFSH;
KW human follicle-stimulating hormone.

XX
OS Homo sapiens.

XX
PN WO200266984-A2.

XX
PD 29-AUG-2002.

XX
PF 15-FEB-2002; 2002WO-NL000097.

XX
PR 16-FEB-2001; 2001EP-00200551.

XX
PA (PEPS-) PEPSCAN SYSTEMS BV.

XX
PI Puijk WC, Van Dijk E, Slootstra JW;

XX
DR WPI; 2003-103161/09.

XX
PT Novel support used for micro-arrays and its use in detection of (bio)
PT molecules.

XX
PS Example 3; Fig 6C; 41pp; English.

XX
CC The present invention relates to a method for the detection of
CC biomolecules in pixel arrays and the supports used for the micro-arrays.
CC The novel supports for the micro-arrays are suitable for determining the
CC binding of a first member molecule within a library of spots of tentative
CC first member binding molecules with a second member binding molecule. The
CC support is provided with a support surface where surface patches are
CC interspersed with surface areas that are materially distinct from the
CC patches. The support and method of the invention are useful for
CC identifying or obtaining a synthetic molecule comprising a binding site,
CC or a binding molecule capable of binding to a binding site. The molecule
CC is useful for interfering with, or effecting binding to a binding
CC molecule. The novel support for a micro-array and the method provide high
CC density arraying (testing many binding events in one go) and enzyme-
CC linked-assays (very sensitive) allowing the detection of more binding
CC pairs more rapidly. ABU14255-ABU14437 represent human follicle-
CC stimulating hormone (hFSH) derived peptides containing a C- or N-terminal
CC cysteine. These peptides are used in the method of the present invention

XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 1 FCISINTTW 9

RESULT 41

ABU14172

ID ABU14172 standard; peptide; 12 AA.

XX
AC ABU14172;

XX
DT 28-FEB-2003 (first entry)

XX DE N-terminal bromoacetamide containing hFSH peptide #99.
XX KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW human follicle-stimulating hormone; hFSH.
XX OS Homo sapiens.
XX PN WO200266984-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-NL000097.
XX PR 16-FEB-2001; 2001EP-00200551.
XX PA (PEPS-) PEPSCAN SYSTEMS BV.
XX PI Puijk WC, Van Dijk E, Slootstra JW;
XX WPI; 2003-103161/09.
XX DR Novel support used for micro-arrays and its use in detection of (bio) molecules.
XX PT Example 3; Fig 6B; 4lpp; English.
XX PS The present invention relates to a method for the detection of biomolecules in pixel arrays and the supports used for the micro-arrays. The novel supports for the micro-arrays are suitable for determining the binding of a first member molecule within a library of spots of tentative first member binding molecules with a second member binding molecule. The support is provided with a support surface where surface patches are interspersed with surface areas that are materially distinct from the patches. The support and method of the invention are useful for identifying or obtaining a synthetic molecule comprising a binding site, or a binding molecule capable of binding to a binding site. The molecule is useful for interfering with, or effecting binding to a binding molecule. The novel support for a micro-array and the method provide high density arraying (testing many binding events in one go) and enzyme-linked-assays (very sensitive) allowing the detection of more binding pairs more rapidly. ABU14074-ABU14254 represent human follicle-stimulating hormone (hFSH) derived peptides containing an N-terminal bromoacetamide group. These peptides are used in the method of the present invention
XX SQ Sequence 12 AA;
Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.le+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 FITTVKTAW 10
| :: |
Db 2 FCISINTTW 10
RESULT 42
ABU14353
ID ABU14353 standard; peptide; 12 AA.
XX AC ABU14353;
XX DT 12-MAR-2003 (first entry)
XX DE C- or N-terminal cysteine containing hFSH peptide #99.
XX KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; hFSH;
KW human follicle-stimulating hormone.

XX OS Homo sapiens.
XX PN WO200266984-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-NL000097.
XX PR 16-FEB-2001; 2001EP-00200551.
XX PA (PEPS-) PEPSCAN SYSTEMS BV.
XX PI Puijk WC, Van Dijk E, Slootstra JW;
XX WPI; 2003-103161/09.
XX PT Novel support used for micro-arrays and its use in detection of (bio) molecules.
XX PS Example 3; Fig 6C; 4lpp; English.
XX CC The present invention relates to a method for the detection of biomolecules in pixel arrays and the supports used for the micro-arrays. The novel supports for the micro-arrays are suitable for determining the binding of a first member molecule within a library of spots of tentative first member binding molecules with a second member binding molecule. The support is provided with a support surface where surface patches are interspersed with surface areas that are materially distinct from the patches. The support and method of the invention are useful for identifying or obtaining a synthetic molecule comprising a binding site, or a binding molecule capable of binding to a binding site. The molecule is useful for interfering with, or effecting binding to a binding molecule. The novel support for a micro-array and the method provide high density arraying (testing many binding events in one go) and enzyme-linked-assays (very sensitive) allowing the detection of more binding pairs more rapidly. ABU14255-ABU14437 represent human follicle-stimulating hormone (hFSH) derived peptides containing a C- or N-terminal cysteine. These peptides are used in the method of the present invention
XX SQ Sequence 12 AA;
Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.le+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 FITTVKTAW 10
| :: |
Db 3 FCISINTTW 11
RESULT 43
ABU14173
ID ABU14173 standard; peptide; 12 AA.
XX AC ABU14173;
XX DT 28-FEB-2003 (first entry)
XX DE N-terminal bromoacetamide containing hFSH peptide #100.
XX KW Biomolecule detection; pixel array; micro-array support;
KW molecule binding; binding molecule; support surface; surface patch;
KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW human follicle-stimulating hormone; hFSH.
XX OS Homo sapiens.
XX PN WO200266984-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-NL000097.

XX 16-FEB-2001; 2001EP-00200551.
XX (PEPS-) PEPSCAN SYSTEMS BV.
XX Puijk WC, Van Dijk E, Slootstra JW;
XX WPI; 2003-103161/09.
XX Novel support used for micro-arrays and its use in detection of (bio)
XX molecules.
XX Example 3; Fig 6B; 41pp; English.
XX The present invention relates to a method for the detection of
XX biomolecules in pixel arrays and the supports used for the micro-arrays.
XX The novel supports for the micro-arrays are suitable for determining the
XX binding of a first member molecule within a library of spots of tentative
XX first member binding molecules with a second member binding molecule. The
XX support is provided with a support surface where surface patches are
XX interspersed with surface areas that are materially distinct from the
XX patches. The support and method of the invention are useful for
XX identifying or obtaining a synthetic molecule comprising a binding site,
XX or a binding molecule capable of binding to a binding site. The molecule
XX is useful for interfering with, or effecting binding to a binding
XX molecule. The novel support for a micro-array and the method provide high
XX density arraying (testing many binding events in one go) and enzyme-
XX linked-assays (very sensitive) allowing the detection of more binding
XX pairs more rapidly. ABU14074-ABU14254 represent human follicle-
XX stimulating hormone (hFSH) derived peptides containing an N-terminal
XX bromoacetamide group. These peptides are used in the method of the
XX present invention
XX Sequence 12 AA;
SQ
Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 FITTVKTAW 10
Db 1 FCISINTTW 9
RESULT 44
AAB38907
ID AAB38907 standard; peptide; 13 AA.
XX
AC AAB38907;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #260.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX Human immunodeficiency virus.
XX WO200058438-A2.
XX 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.
XX
PR 29-MAR-1999; 99US-0126938P.
XX
PA (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX
PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
DR WPI; 2000-656164/63.
XX
XX Synthetic peptides useful for preventing and treating HIV infection in
XX mammals, comprising a conformationally constrained portion and a portion
XX with continuous stretch of amino acids of predicted secondary structure.
XX Disclosure; Page 26; 69pp; English.
XX The present invention relates to peptides (AAB38648-B38970) comprising a
XX first conformationally constrained portion with a cross-linked group of a
XX HIV envelope protein that induces neutralising antibodies, and a second
XX portion comprising a continuous stretch of at least 5 amino acids having
XX a predicted secondary structure. The present sequence is one such
XX peptide. The peptides of the present invention are useful as a vaccine
XX for prophylactic or therapeutic treatment of a mammal for HIV infection
XX Sequence 13 AA;
SQ
Query Match 43.6%; Score 24; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 4 TTVK--TAW 10
Db 3 TTVKWNNTTW 11
RESULT 45
AAB38843
ID AAB38843 standard; peptide; 13 AA.
XX
AC AAB38843;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #196.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX Human immunodeficiency virus.
XX WO200058438-A2.
XX 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.
XX
PR 29-MAR-1999; 99US-0126938P.
XX
PA (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX
PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
DR WPI; 2000-656164/63.
XX
XX Synthetic peptides useful for preventing and treating HIV infection in
XX mammals, comprising a conformationally constrained portion and a portion
XX with continuous stretch of amino acids of predicted secondary structure.
XX Disclosure; Page 24; 69pp; English.
XX The present invention relates to peptides (AAB38648-B38970) comprising a
XX first conformationally constrained portion with a cross-linked group of a
XX HIV envelope protein that induces neutralising antibodies, and a second
XX portion comprising a continuous stretch of at least 5 amino acids having
XX a predicted secondary structure. The present sequence is one such
XX peptide. The peptides of the present invention are useful as a vaccine
XX for prophylactic or therapeutic treatment of a mammal for HIV infection
XX Sequence 13 AA;
SQ

DR WPI; 2000-656164/63.
XX
PT Synthetic peptides useful for preventing and treating HIV infection in
PT mammals, comprising a conformationally constrained portion and a portion
PT with continuous stretch of amino acids of predicted secondary structure.
XX
PS Disclosure; Page 26; 69pp; English.
XX
CC The present invention relates to peptides (AAB38648-B38970) comprising a
CC first conformationally constrained portion with a cross-linked group of a
CC HIV envelope protein that induces neutralising antibodies, and a second
CC portion comprising a continuous stretch of at least 5 amino acids having
CC a predicted secondary structure. The present sequence is one such
CC peptide. The peptides of the present invention are useful as a vaccine
CC for prophylactic or therapeutic treatment of a mammal for HIV infection
XX
SQ Sequence 13 AA;
Query Match 43.6%; Score 24; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 4 TTVK--TAW 10
Db 3 TTVKWNNTTW 11
RESULT 45
AAB38843
ID AAB38843 standard; peptide; 13 AA.
XX
AC AAB38843;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #196.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX Human immunodeficiency virus.
XX WO200058438-A2.
XX 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.
XX
PR 29-MAR-1999; 99US-0126938P.
XX
PA (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX
PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
DR WPI; 2000-656164/63.
XX
XX Synthetic peptides useful for preventing and treating HIV infection in
XX mammals, comprising a conformationally constrained portion and a portion
XX with continuous stretch of amino acids of predicted secondary structure.
XX Disclosure; Page 24; 69pp; English.
XX The present invention relates to peptides (AAB38648-B38970) comprising a
XX first conformationally constrained portion with a cross-linked group of a
XX HIV envelope protein that induces neutralising antibodies, and a second
XX portion comprising a continuous stretch of at least 5 amino acids having
XX a predicted secondary structure. The present sequence is one such
XX peptide. The peptides of the present invention are useful as a vaccine
XX for prophylactic or therapeutic treatment of a mammal for HIV infection
XX Sequence 13 AA;
SQ

Query Match 43.6%; Score 24; DB 3; Length 13;
Best Local Similarity 66.7%; Pred.No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 4 TTVK--TAW 10
| | | | |
Db 3 TTVKWNITW 11

Search completed: August 30, 2004, 10:49:40
Job time : 17.8986 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 9.62838 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITTVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	43.6	14	8 Q9TEN1	Q9ten1 anas castan
2	24	43.6	14	8 Q9TEN3	Q9ten3 anas gracil
3	23.5	42.7	14	8 Q8HGT1	Q8hgt1 gadus morhu
4	22	40.0	12	12 Q80IG7	Q80ig7 choristoneu
5	21	38.2	13	6 Q18890	Q18890 ateles belz
6	20	36.4	8	2 Q9R9E0	Q9r9e0 bacillus su
7	20	36.4	9	6 Q28093	Q28093 bos taurus
8	19	34.5	8	4 Q15902	Q15902 homo sapien
9	19	34.5	9	8 Q9T2K9	Q9t2k9 spinacia oi
10	18.5	33.6	13	11 Q9QW45	Q9qw45 rattus sp.
11	18	32.7	8	11 Q35835	Q35835 rattus sp.
12	18	32.7	9	2 P83529	P83529 lactobacill
13	18	32.7	11	2 Q9R446	Q9r446 neisseria g
14	18	32.7	12	4 Q16405	Q16405 homo sapien
15	18	32.7	13	10 Q42373	Q42373 solanum tub
16	18	32.7	14	4 Q8IVK4	Q8ivk4 homo sapien

17	17	30.9	9	4 Q99887	Q99887 homo sapien
18	17	30.9	11	8 Q9G356	Q9g356 agama atra
19	17	30.9	13	13 Q90XG9	Q90xg9 gallus gall
20	17	30.9	14	4 Q75692	Q75692 homo sapien
21	16	29.1	8	8 Q9T2W0	Q9t2w0 saccharomyc
22	16	29.1	9	2 Q9R635	Q9r635 chlamydia t
23	16	29.1	9	2 Q9R5M1	Q9r5m1 staphylococ
24	16	29.1	9	4 Q9H3Y3	Q9h3y3 homo sapien
25	16	29.1	9	4 Q15896	Q15896 homo sapien
26	16	29.1	10	6 Q9TRU6	Q9tru6 bos taurus
27	16	29.1	11	2 P83537	P83537 lactobacill
28	16	29.1	12	2 Q46039	Q46039 citrobacter
29	16	29.1	12	10 Q9M433	Q9m433 lotus japon
30	16	29.1	12	10 Q8GSB9	Q8gsb9 lolium pere
31	16	29.1	12	11 Q64242	Q64242 rattus sp.
32	16	29.1	13	2 Q9ZEZ1	Q9zez1 buchnera ap
33	15	27.3	8	8 Q94VC1	Q94vc1 varanus rud
34	15	27.3	8	8 Q94VF6	Q94vf6 varanus job
35	15	27.3	8	8 Q94V88	Q94v88 varanus tri
36	15	27.3	8	8 Q94V91	Q94v91 varanus tim
37	15	27.3	8	8 Q94VE4	Q94ve4 varanus mel
38	15	27.3	8	8 Q94VB2	Q94vb2 varanus sal
39	15	27.3	8	8 Q94VF9	Q94vf9 varanus ind
40	15	27.3	8	8 Q94VA7	Q94va7 varanus sal
41	15	27.3	8	8 Q94VB5	Q94vb5 varanus sal
42	15	27.3	8	11 P70243	P70243 mus musculu
43	15	27.3	9	4 Q9H326	Q9h326 homo sapien
44	15	27.3	9	8 Q9T688	Q9t688 gecko gecko
45	15	27.3	9	8 Q94VD8	Q94vd8 varanus nil

ALIGNMENTS

RESULT 1

Q9TEN1	ID	Q9TEN1	PRELIMINARY;	PRT;	14 AA.
AC	Q9TEN1;				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)				
DE	ATPase 8 (Fragment).				
OS	Anas castanea (Chestnut teal).				
OG	Mitochondrion.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.				
OX	NCBI_TaxID=45631;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kennedy M., Spencer H.G.;				
RT	"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";				
RL	Auk 0:0-0(2000).				
DR	EMBL; AF173494; AAD51052.1; --				
DR	GO; GO:0005739; C:mitochondrion; IEA.				
KW	Mitochondrion.				
FT	NON_TER	1			
SQ	SEQUENCE	14 AA;	1672 MW;	80FB803727F9B871	CRC64;

Query Match 43.6%; Score 24; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ITTVKTAW 10
:|:|:|
Db 2 LTTKPTPW 9

RESULT 2

Q9TEN3	ID	Q9TEN3	PRELIMINARY;	PRT;	14 AA.
AC	Q9TEN3;				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				

```
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase 8 (Fragment).
OS Anas gracilis (Grey teal).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=45630;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennedy M., Spencer H.G.;
RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
RL Auk 0:0-0(2000).
DR EMBL; AF173493; AAD51050.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;

Query Match      43.6%; Score 24; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
Db :|||
2 LTTKPTPW 9

RESULT 3
Q8HGT1 PRELIMINARY; PRT; 14 AA.
AC Q8HGT1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase 8 (Fragment).
OS Gadus morhua (Atlantic cod).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATPRK3;
RA Taylor M.I., Fox C., Rico I., Rico C.;
RT "Species-specific TagMan probes for simultaneous identification of
RT (Gadus morhua L.), haddock (Melanogrammus aeglefinus L.) and whiting
RT (Merlangius merlangus L.).";
RL Mol. Ecol. Notes 2:599-601(2002).
DR EMBL; AF526615; AAN85062.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1753 MW; DAAF852330085E6D CRC64;

Query Match      42.7%; Score 23.5; DB 8; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 3 ITTVKTA-W 10
Db :|||
1 MTTPTAPW 9

RESULT 4
Q80IG7 PRELIMINARY; PRT; 12 AA.
AC Q80IG7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mini-cistron protein.
OS Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV).
```

```
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=208973;
RN [1]
RP SEQUENCE FROM N.A.
RA Carstens E.B.;
RT "Identification and analysis of the CfMNPV P143 gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127530; AAF36457.1; -.
SQ SEQUENCE 12 AA; 1252 MW; C878D87A88B2CDD9 CRC64;

Query Match      40.0%; Score 22; DB 12; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVKT 8
Db :|||
5 FAVTTPRT 12

RESULT 5
O18890 PRELIMINARY; PRT; 13 AA.
ID O18890;
AC O18890;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Granzyme B (Fragment).
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98267189; PubMed=9601975;
RA Canavez F., Moreira M.A.M., Bonvicino C.R., Parham P., Seuanez H.N.;
RT "Comparative gene assignment in Ateles paniscus chamek (Platyrrhini,
RT Primates) and man: association of three separate human syntenic groups
RT and evolutionary considerations.";
RL Chromosoma 107:73-79(1998).
DR EMBL; AF029165; AAB84196.1; -.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1394 MW; COFF86BBF4E5EDDD CRC64;

Query Match      38.2%; Score 21; DB 6; Length 13;
Best Local Similarity 33.3%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
Db :|||
2 FVLTAHCW 10

RESULT 6
Q9R9E0 PRELIMINARY; PRT; 8 AA.
ID Q9R9E0;
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
```

RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.O., de Lencastre H., Piggot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spove is
RT homologous to the mra region of Escherichia coli.";
RL Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 893 MW; EE75A1A33321B1A6 CRC64;

Query Match 36.4%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKTA 9
Db :|||

1 MTTKTS 7

RESULT 7
Q28093
ID Q28093 PRELIMINARY; PRT; 9 AA.
AC Q28093;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytokeratin IV gene upstream region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89231609; PubMed=2469572;
RA Blessing M., Jorcano J.L., Franke W.W.;
RT "Enhancer elements directing cell-type-specific expression of
RT cyokeratin genes and changes of the epithelial cytoskeleton by
RT transfections of hybrid cyokeratin genes.";
RL EMBO J. 8:117-126(1989).
DR EMBL; X14478; CAA32640.1; -.
DR PIR; I46016; I46016.
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1044 MW; 819A22D1B5B32B45 CRC64;

Query Match 36.4%; Score 20; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTVKT 8
Db :|||

5 STVKT 9

RESULT 8
Q15902
ID Q15902 PRELIMINARY; PRT; 8 AA.
AC Q15902;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP7E7A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32081; AAA73892.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 931 MW; 83D699CAB1B1B2C9 CRC64;

Query Match 34.5%; Score 19; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITT 5
Db :|||

1 FVTT 4

RESULT 9
Q9T2K9
ID Q9T2K9 PRELIMINARY; PRT; 9 AA.
AC Q9T2K9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LHC II=LIGHT-harvesting chlorophyll protein II (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373386; PubMed=1894641;
RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.;
RT "Tandem mass spectrometry identifies sites of three post-translational
RT modifications of spinach light-harvesting chlorophyll protein II.
RT Proteolytic cleavage, acetylation, and phosphorylation.";
RL J. Biol. Chem. 266:17584-17591(1991).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1042 MW; 6B5D6DC5B322D1B4 CRC64;

Query Match 34.5%; Score 19; DB 8; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TVKTA 9
Db :|||

3 TVKSA 7

RESULT 10
Q9QW45
ID Q9QW45 PRELIMINARY; PRT; 13 AA.
AC Q9QW45;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE GTP-binding protein RAB16 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054572; PubMed=1429617;
RA Elferink L.A., Anzai K., Scheller R.H.;
RT "rabi5, a novel low molecular weight GTP-binding protein specifically
RT expressed in rat brain.";
RL J. Biol. Chem. 267:22693-22693(1992).
FT NON_TER 1
FT NON_TER 13

SQ SEQUENCE 13 AA; 1584 MW; 40BD5FE7236041A3 CRC64;

Query Match
Best Local Similarity 33.6%; Score 18.5; DB 11; Length 13;
Matches 4; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 TTVKTA-AW 10
| :|| :|
Db 3 TQIKTVSW 10

RESULT 11
O35835 PRELIMINARY; PRT; 8 AA.
AC O35835;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 protein.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
RL NRD convertase, a metalloendopeptidase of the insulinase family.";
DR Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EA1BIADC5A5B6 CRC64;

Query Match
Best Local Similarity 32.7%; Score 18; DB 11; Length 8;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
:: |||
Db 1 MSSATTCW 8

RESULT 12
P83529 PRELIMINARY; PRT; 9 AA.
AC P83529;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RL Lactobacillus sanfranciscensis.";
CC Proteomics 2:765-774(2002).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 15 KDA.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 988 MW; 1031B1B1A729C86B CRC64;

Query Match
Best Local Similarity 32.7%; Score 18; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 9 AA; 988 MW; 1031B1B1A729C86B CRC64;

Query Match
Best Local Similarity 32.7%; Score 18; DB 2; Length 11;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FITTVKTA 9
||| :||
Db 1 FIGNMKAA 8

RESULT 13
Q9R446 PRELIMINARY; PRT; 11 AA.
AC Q9R446;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Carbamoyl-phosphate synthase subunit A (Fragment).
GN CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029363; AAC78453.1; -.
DR EMBL; AF029362; AAC78452.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1178 MW; OC07A8E3DDDD33694 CRC64;

Query Match
Best Local Similarity 32.7%; Score 18; DB 2; Length 11;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FITTVKTA 9
||| :||
Db 1 FIGNMKAA 8

RESULT 14
Q16405 PRELIMINARY; PRT; 12 AA.
AC Q16405;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Estrogen receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140401; PubMed=1779972;
RA Wang Y., Miksicek R.J.;
RT "Identification of a dominant negative form of the human estrogen
RT receptor.";
RL Mol. Endocrinol. 5:1707-1715(1991).
DR EMBL; S79911; AAB21301.1; -.
DR PIR; I77529; I77529.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1280 MW; 5A876633B3A37DD3 CRC64;

Query Match 32.7%; Score 18; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
:| |
Db 2 SVTKAW 7

RESULT 15

Q42373 ID Q42373 PRELIMINARY; PRT; 13 AA.
AC Q42373;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Patatin class I (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=88226014; PubMed=3371664;
RX Mignery G.A., Pikaard C.S., Park W.D.;
RA "Molecular characterization of the patatin multigene family of potato."
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON TER 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 32.7%; Score 18; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTV 6
:| |
Db 7 FLITV 12

RESULT 16

Q81VK4 ID Q81VK4 PRELIMINARY; PRT; 14 AA.
AC Q81VK4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Steerin2 protein (Fragment).
GN STEERIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.;
RA Geysen J.J.G.H.;
RT "Sensorineural defects in mice hypomorphic for a mammalian homolog of unc-53."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ488207; CAD32560.1; -.
FT NON TER 14
SQ SEQUENCE 14 AA; 1267 MW; C67BE72BA83F9CBD CRC64;

Query Match 32.7%; Score 18; DB 4; Length 14;
Best Local Similarity 28.6%; Pred. No. 1.2e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTAW 10

Db 4 TSAASSW 10

RESULT 17

Q99887 ID Q99887 PRELIMINARY; PRT; 9 AA.
AC Q99887;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE 11 <beta>-HSD2 protein (Fragment).
GN 11 <BETA>-HSD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=96133030; PubMed=8538347;
RX Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,
RA Sheppard M.C., Whorwood C.B.;
RT "Hypertension in the syndrome of apparent mineralocorticoid excess due to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene."
RL Lancet 347:88-91(1996).
DR EMBL; S80133; AAD14324.1; -.
DR GO; GO:0003845; F:11-beta-hydroxysteroid dehydrogenase activity; NAS.
DR GO; GO:0008212; P:mineralocorticoid metabolism; NAS.
FT NON TER 1
SQ SEQUENCE 9 AA; 1020 MW; CEF2C2EB1F5B059C9 CRC64;

Query Match 30.9%; Score 17; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFIT 4
:| |
Db 2 FFIS 5

RESULT 18

Q9G356 ID Q9G356 PRELIMINARY; PRT; 11 AA.
AC Q9G356;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Agama atra (Southern rock agama).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
OX NCBI_TaxID=52208;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs."
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]_SEQUENCE FROM N.A.
RP MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).
RN [3]_SEQUENCE FROM N.A.
RP MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

```
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128505; AAG00752.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1402 MW; B052EC10D36411A6 CRC64;

Query Match
Best Local Similarity 30.9%; Score 17; DB 8; Length 11;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
Db | | |
2 TKWTRW 7

RESULT 19
Q90XG9 PRELIMINARY; PRT; 13 AA.
AC Q90XG9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pdc4 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363043; PubMed=11470166;
RA Schlichter U., Kattmann D., Appl H., Miethe J., Brehmer-Fastnacht A.,
RA Klempnauer K.-H.;
RT "Identification of the myb-inducible promoter of the chicken Pdc4
RT gene.";
RL Biochim. Biophys. Acta 1520:99-104(2001).
DR EMBL; AF382032; AAK59968.1; -.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1577 MW; DF23FEC8057BC1F6 CRC64;

Query Match
Best Local Similarity 30.9%; Score 17; DB 13; Length 13;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITTV 6
Db :|:|
9 YISTV 13

RESULT 20
O75692 PRELIMINARY; PRT; 14 AA.
AC O75692;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN GTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Visvikis A.;
RT "Identification of promoter sequences driving the expression of type
RT III human gamma-glutamyltransferase mRNAs.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006789; CAA07253.1; -.
KW Hypothetical protein.
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FT NON TER 14 14
SQ SEQUENCE 14 AA; 1641 MW; D8CE5693986DE4C2 CRC64;

Query Match
Best Local Similarity 30.9%; Score 17; DB 4; Length 14;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
Db ||:
5 FFVAQLR 11

RESULT 21
Q9T2W0 PRELIMINARY; PRT; 8 AA.
AC Q9T2W0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CBS1 PRECURSOR=PROTEOLYTIC processing site (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=92035078; PubMed=1657414;
RA Korte A., Michaelis U., Lottspeich F., Rodel G.;
RT "Over-expression, purification and determination of the proteolytic
RT processing site of the yeast mitochondrial CBS1 protein.";
RL Curr. Genet. 20:87-90(1991).
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 913 MW; 72D1A44041B40047 CRC64;

Query Match
Best Local Similarity 29.1%; Score 16; DB 8; Length 8;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKT 8
Db ||:
2 IRTINT 7

RESULT 22
Q9R635 PRELIMINARY; PRT; 9 AA.
AC Q9R635;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major outer membrane protein variable domain IV, MOMP VD IV
DE (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92040090; PubMed=1718870;
RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
RT "Functional and structural mapping of Chlamydia trachomatis species-
RT specific major outer membrane protein epitopes by use of neutralizing
RT monoclonal antibodies.";
RL Infect. Immun. 59:4147-4153(1991).
DR PIR; S16034; S16034.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;

Query Match
Best Local Similarity 29.1%; Score 16; DB 2; Length 9;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 8 TAW 10
| |
1 TTW 3

Db

RESULT 23

Q9R5M1 PRELIMINARY; PRT; 9 AA.

ID Q9R5M1

AC Q9R5M1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RP SEQUENCE.

RX MEDLINE=92176005; PubMed=1541563;

RA Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;

RT "Binding of heparan sulfate to Staphylococcus aureus.";

RL Infect. Immun. 60:899-906(1992).

DR PIR; A43848; A43848. 1

FT NON_TER 1

FT NON_TER 9

SQ SEQUENCE 9 AA; 990 MW; 2289DDD7337861B3 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
| |
3 TGW 5

Db

RESULT 24

Q9H3Y3 PRELIMINARY; PRT; 9 AA.

ID Q9H3Y3

AC Q9H3Y3;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE DJ839B11.1 (Novel protein with a kunitz/bovine pancreatic trypsin inhibitor domain and WAP-type (Whey acidic protein) 'four-disulfide core' domains) (Fragment).

DE core' domains) (Fragment).

GN DJ461P17.1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Lloyd D.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL121778; CAB76844.1; -.

FT NON_TER 9

SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TVKT 8
| |
3 TVRT 6

Db

RESULT 25

Q15896 PRELIMINARY; PRT; 9 AA.

ID Q15896

AC Q15896;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE (Clone XP6A10B) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,

RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of

RT arrayed cDNAs and cosmid libraries.";

RL Hum. Mol. Genet. 0:0-0(1995).

DR EMBL; L32076; AAA73886.1; -.

FT NON_TER 1

FT NON_TER 9

SQ SEQUENCE 9 AA; 1047 MW; 11D15731B2C9C054 CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FITTV 6
| |
4 FVTLI 8

Db

RESULT 26

Q9TRU6 PRELIMINARY; PRT; 10 AA.

ID Q9TRU6

AC Q9TRU6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE GAP-3, GTPase-activating protein (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=92112868; PubMed=1309786;

RA Nice B.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,

RA Burgess A.W.;

RT "The purification of a Rap1 GTPase-activating protein from bovine

RT brain cytosol.";

RL J. Biol. Chem. 267:1546-1553(1992).

FT NON_TER 1

FT NON_TER 10

SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 29.1%; Score 16; DB 6; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| |
1 FLLTKLTNA 9

Db

RESULT 27

P83537 PRELIMINARY; PRT; 11 AA.

ID P83537

AC P83537;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Unknown protein from 2D-page (Fragment).

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20427395; PubMed=10975655;
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 65 KDA.
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFIT 4
Db 3 FFAT 6

RESULT 28
Q46039
ID Q46039 PRELIMINARY; PRT; 12 AA.
AC Q46039;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FrdB protein (Fragment).
GN FRDB.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89291719; PubMed=2786868;
RA Lindquist S., Lindberg F., Normark S.;
RT "Binding of the Citrobacter freundii AmpR regulator to a single DNA
RT site provides both autoregulation and activation of the inducible ampC
RT beta-lactamase gene."
RL J. Bacteriol. 171:3746-3753(1989).
DR EMBL; M27222; AAA64511.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 12 AA; 1214 MW; 968D697A24705DC1 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TVKTA 9
Db 2 TVVTA 6

RESULT 29
Q9M433
ID Q9M433 PRELIMINARY; PRT; 12 AA.
AC Q9M433;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENOD40-1 protein.
GN ENOD40-1.
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20427395; PubMed=10975655;
RA Fletetakis E., Kavroulakis N., Quaedvlieg N.E.M., Spaink H.P.,
RA Dimou M., Roussis A., Katinakis P.;
RT "Lotus japonicus contains two distinct ENOD40 genes that are expressed
RT in symbiotic, non-symbiotic and embryonic tissues.";
RL Mol. Plant Microbe Interact. 13:987-994(2000).
DR EMBL; AJ271787; CAB92978.1; -.
SQ SEQUENCE 12 AA; 1403 MW; 3C6955187CB046C3 CRC64;

Query Match 29.1%; Score 16; DB 10; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 1 MKLCW 5

RESULT 30
Q8GSB9
ID Q8GSB9 PRELIMINARY; PRT; 12 AA.
AC Q8GSB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENOD40-like protein.
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Borvi; TISSUE=Stem;
RA Larsen K.;
RT "ENOD40 homolog from perennial ryegrass (Lolium perenne).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Larsen K.;
RT "ENOD40 gene from perennial ryegrass (Lolium perenne).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538350; AAN15133.1; -.
DR EMBL; AF538351; AAN15134.1; -.
SQ SEQUENCE 12 AA; 1455 MW; 3EF4B0A918EB1733 CRC64;

Query Match 29.1%; Score 16; DB 10; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.5e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 1 MEDAW 5

RESULT 31
Q64242
ID Q64242 PRELIMINARY; PRT; 12 AA.
AC Q64242;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sodium channel I1la (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92211397; PubMed=1313493;
RA Schaller K.L., Krzemien D.M., McKenna N.M., Caldwell J.H.;
RT "Alternatively spliced sodium channel transcripts in brain and
RT muscle.";
RL J. Neurosci. 12:1370-1381(1992).
DR EMBL; S97387; AAB21983.2; --
DR PIR; A44824; A44824.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1238 MW; 9C79B13247A866C5 CRC64;

Query Match 29.1%; Score 16; DB 11; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTVKT 8
|||
Db 8 TTET 12

RESULT 32
Q9ZEZ1 PRELIMINARY; PRT; 13 AA.
AC Q9ZEZ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OG Plasmid pBPl.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006877; CA07302.1; --
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1538 MW; 1BD1D0320390C050 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FITTVK 7
|||
Db 8 FDTTLR 13

RESULT 33
Q94VC1 PRELIMINARY; PRT; 8 AA.
AC Q94VC1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus rudicollis (Rough-necked monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169851;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407521; AAL10116.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
|||
Db 2 TRW 4

RESULT 34
Q94VF6 PRELIMINARY; PRT; 8 AA.
AC Q94VF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus jobiensis (Peach throat monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169843;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407507; AAL10075.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1144 MW; EFD729DB436411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
|||
Db 2 TRW 4

RESULT 35
Q94V88 PRELIMINARY; PRT; 8 AA.
AC Q94V88;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus tristis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62052;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;

```
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407533; AAL10151.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match
Best Local Similarity 27.3%; Score 15; DB 8; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
2 TRW 4

RESULT 36
Q94V91
ID Q94V91 PRELIMINARY; PRT; 8 AA.
AC Q94V91;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus timorensis (Timor monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62053;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407532; AAL10148.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match
Best Local Similarity 27.3%; Score 15; DB 8; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
2 TRW 4

RESULT 37
Q94VE4
ID Q94VE4 PRELIMINARY; PRT; 8 AA.
AC Q94VE4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus melinus (Quince monitor lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169846;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407511; AAL10087.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
```

```
FT NON TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match
Best Local Similarity 27.3%; Score 15; DB 8; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
2 TRW 4

RESULT 38
Q94VB2
ID Q94VB2 PRELIMINARY; PRT; 8 AA.
AC Q94VB2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus salvator togianus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169832;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407524; AAL10125.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match
Best Local Similarity 27.3%; Score 15; DB 8; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
2 TRW 4

RESULT 39
Q94VF9
ID Q94VF9 PRELIMINARY; PRT; 8 AA.
AC Q94VF9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus indicus (Mangrove monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62043;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407506; AAL10072.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match
Best Local Similarity 27.3%; Score 15; DB 8; Length 8;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
2 TRW 4
```

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 40

Q94VA7 PRELIMINARY; PRT; 8 AA.
ID Q94VA7
AC Q94VA7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus salvator salvator.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169831;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407526; AAL10130.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 41

Q94VB5 PRELIMINARY; PRT; 8 AA.
ID Q94VB5;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus salvator cumingi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169830;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407523; AAL10122.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 42

Q9H326 PRELIMINARY; PRT; 9 AA.
ID Q9H326
AC Q9H326;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit (Fragment).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1; --
FT NON TER 9
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 27.3%; Score 15; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10

Db 5 AW 6

RESULT 43

Q9H326 PRELIMINARY; PRT; 9 AA.
ID Q9H326
AC Q9H326;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit (Fragment).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1; --
FT NON TER 9
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 27.3%; Score 15; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10

Db 5 AW 6

RESULT 44

Q9T688 PRELIMINARY; PRT; 9 AA.
ID Q9T688
AC Q9T688;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)


```
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Gecko gecko (Tokay gecko).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gecko.
OX NCBI_TaxID=36310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343618; PubMed=10413626;
RA Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
RT "Vicariant patterns of fragmentation among gekkonid lizards of the
RT genus teratascincus produced by the indian collision: A molecular
RT phylogenetic perspective and an area cladogram for central asia.";
RL Mol. Phylogenet. Evol. 12:320-332(1999).
DR EMBL; AF114249; AAD51600.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 9
SQ SEQUENCE 9 AA; 1188 MW; 428CB9C9D36411A7 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFIT 4
Db |||
6 FFST 9

RESULT 45
Q94VD8
ID Q94VD8 PRELIMINARY; PRT; 9 AA.
AC Q94VD8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus niloticus (Nile monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407514; AAL10096.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 9
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db |||
4 TRW 6
```

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.72297 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFTTVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	30.9	9	1	PTSP_BOMMO
2	17	30.9	10	1	LABA_JATMU
3	16	29.1	8	1	AKHG_GRYBI
4	16	29.1	10	1	CA12_LITCI
5	16	29.1	10	1	CAER_LITXA
6	16	29.1	10	1	HTF_HELZE
7	16	29.1	11	1	CA31_LITCI
8	16	29.1	11	1	CA32_LITCI
9	16	29.1	12	1	CX41_CONIM
10	16	29.1	12	1	NO40_SESRO
11	16	29.1	12	1	NO40_SOYBN
12	16	29.1	12	1	UH03_RAT
13	16	29.1	12	1	V25K_WSSV
14	16	29.1	14	1	NEJ2_FASHE
15	15	27.3	8	1	RT34_BOVIN
16	15	27.3	9	1	LMIP_LOCFI
17	15	27.3	10	1	TKNK_PIG
18	15	27.3	10	1	TPIS_NICPL
19	15	27.3	12	1	YZPY_ECOLI
20	15	27.3	13	1	EI21_LITRU
21	15	27.3	13	1	EI22_LITRU
22	15	27.3	13	1	UHA3_CANFA
23	15	27.3	14	1	ALYT_ALYOB
24	15	27.3	14	1	LPF2_ECOLI
25	15	27.3	14	1	UC04_MAIZE
26	14	25.5	8	1	PLP_BRANA
27	14	25.5	12	1	PORD_METTM
28	14	25.5	13	1	YPNP_PHOLU
29	14	25.5	14	1	CX1A_CONBE
30	14	25.5	14	1	LPW_CITFR
31	14	25.5	14	1	LPW_ECOLI
32	13	23.6	8	1	AKH_TABAT
33	13	23.6	8	1	LCK2_LEUMA

34	13	23.6	8	1	LCK5_LEUMA	P19987 leucophaea
35	13	23.6	8	1	LCK7_LEUMA	P19989 leucophaea
36	13	23.6	10	1	APE_CAPGI	P80474 capnocytoph
37	13	23.6	10	1	COXQ_SHEEP	P80337 ovis aries
38	13	23.6	10	1	HTF_TABAT	P14596 tabanus atr
39	13	23.6	12	1	UR2_POLSP	P81022 polyodon sp
40	13	23.6	13	1	LIGB_TRAVE	P20012 trametes ve
41	13	23.6	13	1	TY13_PHYRO	P04096 phyllomedus
42	13	23.6	14	1	KARA_BROPL	P22442 bromelia pl
43	13	23.6	14	1	MCRX_METTM	P58815 methanobact
44	13	23.6	14	1	SMS1_MYOSC	P20750 myoxocephal
45	13	23.6	14	1	SMS_ALLMI	P31885 alligator m

ALIGNMENTS

RESULT 1
PTSP_BOMMO STANDARD; PRT; 9 AA.
AC P82003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prothoracicostatic peptide (Bom-PTSP).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=C145 X N140; TISSUE=Brain;
RX MEDLINE=20002634; PubMed=10531308;
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA Kataoka H.;
RT "Identification of a prothoracicostatic peptide in the larval brain of
the silkworm, Bombyx mori.";
RL J. Biol. Chem. 274:31169-31173(1999).
RN [2]
RP ERRATUM.
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA Kataoka H.;
RL J. Biol. Chem. 275:9892-9892(2000).
CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
gland.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: Early fifth instar.
KW Hormone; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
: :|||
DB 5 LNSAW 9

RESULT 2
LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Labaditin.
OS Jatropa multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;

OC Jatropa.
OX NCBI_TaxID=3996;
RN [1] _____
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapetide from the latex of Jatropa
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
CC classical pathway of complement activation in vitro. Activity
CC seems to be based on an interaction with C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
CC for treatment of infected wounds, skins infections and scabies.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db [1] _____
3 VWTWV 7

RESULT 3
AKHG_GRYBI STANDARD; PRT; 8 AA.
ID AKHG_GRYBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1] _____
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2] _____
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db [1] _____
6 TGV 8

RESULT 4
CA12_LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770, 30345;
RN [1] _____
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
RC SPECIES=L.citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN [2] _____
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendipherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10.";
RL Eur. J. Biochem. 267:269-275(2000).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db [1] _____
5 TGV 7

RESULT 5
CAER_LITXA STANDARD; PRT; 10 AA.
ID CAER_LITXA
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
RT Australian tree frog Litoria xanthomera."
RL J. Pept. Sci. 3:181-185(1997).
CC -!- FUNCTION: Hypotensive neuropeptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861BB5A CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
DB 5 TGW 7

RESULT 6
HTP_HELZE
ID HTP_HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (HeZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosemic and adipokinetic activities."
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A31571; A31571.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
DB 3 TFSGW 8

RESULT 7
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 29.1%; Score 16; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
DB 6 TGW 8

RESULT 8
CA32_LITCI
ID CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;

```
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT contains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 29.1%; Score 16; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db | |
6 TGW 8

RESULT 9
CXAL_CONIM STANDARD; PRT; 12 AA.
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin ImI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=35631;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=94266889; PubMed=8206995;
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
RA Gray W.R., Olivera B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin ImI.";
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
RA McIntosh J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; PubMed=10194298;
RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
RA Wenner D.E.;
RT "NMR solution structure of alpha-conotoxin ImI and comparison to
RT other conotoxins specific for neuronal nicotinic acetylcholine
RT receptors.";
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=99280313; PubMed=10350614;
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RA Gouda H., Hirono S.;
RT "Solution structure of alpha-conotoxin ImI determined by
RT two-dimensional NMR spectroscopy.";
RL Biochim. Biophys. Acta 1431:384-394(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; PubMed=10050774;
RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
RT scaffold in snail and snake toxins recognizing neuronal nicotinic
RT acetylcholine receptors.";
RL FEBS Lett. 444:275-280(1999).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=99358772; PubMed=10431825;
RA Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;
RT "Minimal conformation of the alpha-conotoxin ImI for the alpha7
RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,
RT NMR and binding studies.";
RL FEBS Lett. 454:293-298(1999).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; PubMed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin ImI by 1H nuclear magnetic
RT resonance.";
RL J. Med. Chem. 42:2364-2372(1999).
RN [8]
RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
RP THREE MUTANTS.
RX MEDLINE=20574023; PubMed=11124036;
RA Rogers J.P., Luginbuhl P., Pemberton K., Harty P., Wenner D.E.,
RA Stevens R.C.;
RT "Structure-activity relationships in a peptidic alpha7 nicotinic
RT acetylcholine receptor antagonist.";
RL J. Mol. Biol. 304:911-926(2000).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. It is highly active against the neuromuscular
CC receptor in frog but not in mice. In contrast, it induces seizures
CC when injected centrally in mice and rats. It targets neuronal
CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
CC with the highest apparent affinity and homomeric alpha-9 receptors
CC with 8-fold lower affinity. It has no effect on receptors composed
CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A53709; A53709.
DR PDB; 1CNL; 27-MAY-99.
DR PDB; 1E74; 27-DEC-00.
DR PDB; 1E75; 27-DEC-00.
DR PDB; 1E76; 27-DEC-00.
DR PDB; 1G2G; 08-NOV-00.
DR PDB; 1IM1; 15-JUN-99.
DR PDB; 1IMI; 23-APR-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 12
FT MOD_RES 12 12 AMIDATION.
FT MUTAGEN 5 5 D->L: REDUCTION OF TOXICITY.
FT MUTAGEN 7 7 R->L: REDUCTION OF TOXICITY.
FT MUTAGEN 11 11 R->E: NO LOSS OF ACTIVITY.
FT HELIX 2 4
FT HELIX 6 8
FT TURN 10 12
SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
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Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
Db : ||
7 RCAW 10

RESULT 10
NO40_SESRO STANDARD; PRT; 12 AA.
AC O24369;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Early nodulin 40.
GN ENOD40.
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem nodules;
RX MEDLINE=98281575; PubMed=9620265;
RA Corich V., Goormachtig S., Lievens S., van Montagu M., Holsters M.;
RT "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania rostrata.";
RL Plant Mol. Biol. 37:67-76(1998).
CC -!- FUNCTION: Modulates the action of auxin, and may function as plant growth regulator that alters phytohormone responses (By similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in the early stages of the nodule development.
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DR EMBL; Y12714; CAA73252.1; -.
KW Nodulation.
SQ SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db : ||
1 MKLCW 5

RESULT 11
NO40_SOYBN STANDARD; PRT; 12 AA.
AC P55960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
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```
STRAIN=cv. Williams;
RX MEDLINE=94035161; PubMed=8220464;
RA Yang W.C., Katinakis P., Hendriks P., Smolders A., de Vries F.,
RA Spee J., van Kammen A., Bisseling T., Franssen H.;
RT "Characterization of GmENOD40, a gene showing novel patterns of cell-specific expression during soybean nodule development.";
RL Plant J. 3:573-585(1993).
CC -!- FUNCTION: Modulates the action of auxin, and may function as plant growth regulator that alters phytohormone responses (By similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in the early stages of the nodule development.
-----
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DR EMBL; X69154; -; NOT_ANNOTATED_CD.
KW Nodulation.
SQ SEQUENCE 12 AA; 1391 MW; 3C6958AE78B1A733 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITTV 6
Db : ||:
5 WLTTI 9

RESULT 12
UH03_RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 8.3, its MW is: 28 kDa.
FT UNSURE 2 2
FT UNSURE 9 9
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTA 9
Db : ||
4 TKIKVA 9

RESULT 13
V25K_WSSV STANDARD; PRT; 12 AA.
ID V25K_WSSV
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polyprotein (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus."
RT virus."
RL Arch. Virol. 145:263-274 (2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FTTVTKTA 9
| : | |
Db 5 FTLSVVTA 12

RESULT 14
NEJ2_FASHE
ID NEJ2_FASHE STANDARD; PRT; 14 AA.
AC P80526;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Newly excysted juvenile protein 2 (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcovic J., Ashman K., Meeusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile proteins."
RT Biochem. Biophys. Res. Commun. 213:169-174 (1995).
RL -!- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile stage.
CC NON_TER 14 14
FT SEQUENCE 14 AA; 1581 MW; 9E0F0090CC8C0DF1 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
: | |
Db 6 RTHW 9

RESULT 15
RT34_BOVIN
ID RT34_BOVIN STANDARD; PRT; 8 AA.
AC P82929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
GN MRPS34.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins present."
RL J. Biol. Chem. 276:19363-19374 (2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 27.3%; Score 15; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
| |
Db 1 AW 2

RESULT 16
LMIP_LOCMI
ID LMIP_LOCMI STANDARD; PRT; 9 AA.
AC P31799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyo-inhibiting peptide (LOM-MIP).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyo-inhibiting peptide (LOM-MIP), a novel biologically active neuro-peptide from Locusta migratoria."
RT Regul. Pept. 36:111-119 (1991).
RL -!- FUNCTION: Suppresses spontaneous contractions of the hindgut and oviduct.
CC -!- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters in the suboesophageal ganglion.
CC PIR; A60065; AKLQIM.
KW Amidation; Neuro-peptide.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
| |
Db 1 AW 2

RESULT 17
TKNK_PIG
ID TKNK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).

GN TAC3 OR NKNB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01560; SPPGNK.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAA1 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
Db ||:
5 FFV 7

RESULT 18
TPIS_NICPL
ID TPIS_NICPL STANDARD; PRT; 10 AA.
AC P191I8;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically separated from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: In plants, there are two types of TPIS, cytosolic
CC and plastid.
CC -!- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR PIR; A27617; A27617.

DR InterPro; IPR000652; Triophos ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
Db ||:
4 FFV 6

RESULT 19
YZPY_ECOLI
ID YZPY_ECOLI STANDARD; PRT; 12 AA.
AC P17776;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Hypothetical pyrE leader peptide.
GN PYRL OR PYRE-LP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85003588; PubMed=6207018;
RA Poulsen P., Bonekamp F., Jensen K.F.;
RT "Structure of the Escherichia coli pyrE operon and control of pyrE
RT expression by a UTP modulated intercistronic attenuation.";
RL EMBO J. 3:1783-1790(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83287414; PubMed=6349999;
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
RA Lundberg L.G.;
RT "Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA
RT in front of the protein-coding region.";
RL Eur. J. Biochem. 135:223-229(1983).
CC -!- CAUTION: This sequence, according to the EcoSeq database (K. Rudd)
CC is probably not a real protein; therefore this entry will probably
CC be deleted in future releases.
CC -----
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CC -----
DR EMBL; X00781; -; NOT_ANNOTATED_CDS.
DR EMBL; V01578; -; NOT_ANNOTATED_CDS.
DR PIR; A30400; LFECPE.
KW Hypothetical protein.
SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
Db ||:
5 FFV 7

RESULT 20

```
EI21_LITRU
ID EI21_LITRU STANDARD; PRT; 13 AA.
AC P82097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 5 KVKW 8

RESULT 21
EI22_LITRU
ID EI22_LITRU STANDARD; PRT; 13 AA.
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 5 KVKW 8
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UHA3_CANFA STANDARD; PRT; 13 AA.
ID P56535;
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.9, its MW is: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FIT 4
Db 3 FIT 5

RESULT 23
ALYT_ALYOB
ID _ALYT_ALYOB STANDARD; PRT; 14 AA.
AC P08944;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alytesin.
OS Alytes obstetricans (Midwife toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.
OX NCBI_TaxID=8443;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RT "Active peptides in the skins of one hundred amphibian species from
RT Australia and Papua New Guinea.";
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
CC family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db 6 TQW 8
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RESULT 24
LPF2_ECOLI
ID LPF2_ECOLI STANDARD; PRT; 14 AA.
AC P06985;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phenylalanyl-tRNA synthetase operon leader peptide (PheST attenuator
DE peptide).
GN PHEM OR PHTL OR B1715 OR C5495 OR Z2744 OR ECS2422 OR STY1774 OR T1217
GN OR SF1516 OR S4806.
OS Escherichia coli, O6,
OS Escherichia coli O157:H7,
OS Salmonella typhi, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 601, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=85210878; PubMed=3158742;
RA Springer M., Mayaux J.-F., Fayat G., Plumbridge J.A., Graffe M.,
RA Blanquet S., Grunberg-Manago M.;
RT "Attenuation control of the Escherichia coli phenylalanyl-tRNA
RT synthetase operon.";
RL J. Mol. Biol. 181:467-478 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=84090239; PubMed=6317865;
RA Fayat G., Mayaux J.-F., Sacerdot C., Fromant M., Springer M.,
RA Grunberg-Manago M., Blanquet S.;
RT "Escherichia coli phenylalanyl-tRNA synthetase operon region.
RT Evidence for an attenuation mechanism. Identification of the gene for
RT the ribosomal protein L20.";
RL J. Mol. Biol. 171:239-261 (1983).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=88163794; PubMed=3126825;
RA Springer M., Graffe M., Mayaux J.-F., Dardel F., Fayat G.,
RA Blanquet S., Grunberg-Manago M.;
RT "Open reading frames in the control regions of the phenylalanyl-tRNA
RT synthetase operon of E. coli.";
RL Biochimie 69:1065-1070 (1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337 (2003).
RN [10]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441 (2002).
RN [11]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786 (2003).
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CC -----
DR EMBL; M10423; AAA23961.1; -;
DR EMBL; V00291; CAA23563.1; -;
DR EMBL; M13251; AAA24333.1; -;
DR EMBL; AE000266; AAC74785.1; -;
DR EMBL; AE016761; AAN80571.1; -;
DR EMBL; AE005394; AAG56702.1; -;
DR EMBL; AP002558; BAB35845.1; -;
DR EMBL; AL627271; CAD02016.1; -;
DR EMBL; AE016838; AAO68872.1; -;
DR EMBL; AE015174; AAN43106.1; -;
DR EMBL; AE016983; AAP16996.1; -;
DR PIR; B85780; B85780.
DR PIR; F90931; F90931.
DR PIR; S11551; LFECFS.
DR EcoGene; EG11272; pheM.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1762 MW; 7D31C48E0060F0D4 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFTT 5
| : |
Db 10 FYFST 14

RESULT 25
UC04 MAIZE
ID UC04 MAIZE STANDARD; PRT; 14 AA.
AC P80610;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128) (Fragment).
DE Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.8, its MW is: 34.6 kDa.
DR Maize-2DPAGE; P80610; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1393 MW; C14451BA1116D4AD CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVK 7
| : |
Db 5 FSATVR 10

RESULT 26
PLP_BRANA
ID PLP BRANA STANDARD; PRT; 8 AA.
AC P81707;

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of Brassica napus."
RL Planta 208:588-598(1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
| : |
Db 1 VIDVNDW 8

RESULT 27
PORD METTM
ID PORD METTM STANDARD; PRT; 12 AA.
AC P80903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit) (Fragment).
DE GN PORD.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum."
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-CoA + CO(2) + reduced ferredoxin.
CC -!- COFACTOR: Binds 2 4Fe-4S clusters (By similarity).
CC -!- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one gamma chain.
CC -!- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature of 80 degrees Celsius.
CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TVK 7
| : |


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OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA Horowitz H., van Cleemput M., Wu A.M.;
RT "The complete nucleotide sequence of the tryptophan operon of
RT Escherichia coli.";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT Escherichia coli.";
RL J. Mol. Biol. 103:351-381(1976).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
RN [10]
RP FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC EMBL; J01714; AAA57296.1; -
CC EMBL; A04494; CAA00361.1; -
CC EMBL; AE000224; AAC74347.1; -
CC EMBL; AE016760; AAN80196.1; -
CC EMBL; AE005380; AAG56550.1; -
CC EMBL; AP002556; BAB35260.1; -
CC EMBL; AE015153; AAN42881.1; -
CC EMBL; AE016982; AAP16766.1; -
CC PIR; A03589; LFECW.
CC PIR; B85761; B85761.
CC PIR; E90858; E90858.
CC EcoGene; EG11274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;
Query Match 25.5%; Score 14; DB 1; Length 14;
Best Local Similarity 37.5%; Pred.No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 ITTVKTAW 10
Db 4 IFVLKGWW 11
RESULT 32
AKH_TABAT
ID AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
```


RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A33995; A33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TVKTAW 10
Db 3 TFTPGR 8

RESULT 33
LCK2_LEUMA
ID LCK2 LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211 (1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach protodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
Db 5 SSW 7

RESULT 34
LCK5_LEUMA
ID LCK5 LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30 (1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach protodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
Db 5 SSW 7

RESULT 35
LCK7_LEUMA
ID LCK7 LEUMA STANDARD; PRT; 8 AA.
AC P19989;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinins VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34 (1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach protodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDC76A CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
Db 5 SSW 7

RESULT 36
APE_CAPGI
ID APE_CAPGI STANDARD; PRT; 10 AA.


```
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopectidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
RT factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: Requires magnesium or calcium.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 40.0%; Pred.No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 2 VNMLW 6

RESULT 37
COXQ_SHEEP STANDARD; PRT; 10 AA.
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to Swiss-Prot.
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10
FT SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 60.0%; Pred.No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTA 9
Db 2 TAKPA 6
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RESULT 38
HTF TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
FT SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 33.3%; Pred.No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TVKTAW 10
Db 3 TFTPGEW 8

RESULT 39
UR2_POLSP STANDARD; PRT; 12 AA.
AC P81022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Polyodon spathula (North American paddlefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
OC Polyodon.
OX NCBI_TaxID=7913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=96051494; PubMed=8536944;
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula).";
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
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CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the urotensin 2 family.
DR  InterPro; IPR001483; Urotensin II.
DR  Pfam; PF02083; Urotensin_II; 1.
DR  PROSITE; PS00984; UROTENSIN_II; 1.
KW  Hormone.
FT  DISULFID 6 11 BY SIMILARITY.
SQ  SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;

Query Match 23.6%; Score 13; DB 1; Length 12;
Best Local Similarity 28.6%; Pred. No. 1.6e+04;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
Db 2 STSECFW 8

RESULT 40
LIGB_TRAVE STANDARD; PRT; 13 AA.
AC P20012;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ligninase B (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
peroxidase) (Fragment).
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE.
RX MEDLINE=892111432; PubMed=2707445;
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
RT "Trametes versicolor ligninase: isozyme sequence homology and
substrate specificity."
RL FEBS Lett. 247:143-146(1989).
CC -!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
C(beta) cleavage of the propyl side chains of lignin.
CC -!- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol +
H(2)O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol
+ 4 H(2)O.
CC -!- PATHWAY: Lignin degradation; first step.
CC -!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
DR PIR; S04014; S04014.
DR InterPro; IPR002016; Peroxidase.
DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE; PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
KW Multigene family; Lignin degradation.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1269 MW; 22C50ED5872A52C8 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTA 9
Db 7 VNTA 10

RESULT 41
TY13_PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phylomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC  Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC  Phyllomedusinae; Phyllomedusa.
OX  NCBI_TaxID=8394;
RN  [1]
RP  SEQUENCE.
RA  Montecucchi P.C., Gozzini L., Erspamer V.;
RT  "Primary structure determination of a tryptophan-containing
RT  tridecapeptide from Phyllomedusa rohdei."
RL  Int. J. Pept. Protein Res. 27:175-182(1986).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
DR  PIR; A05174; A05174.
KW  Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ  SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 3 KPYW 6

RESULT 42
KARA_BROPL STANDARD; PRT; 14 AA.
AC P22442;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Karatin (EC 3.4.22.-) (Fragment).
OS Bromelia plumieri (Karatas).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
OC Bromelia.
OX NCBI_TaxID=4617;
RN [1]
RP SEQUENCE.
RX MEDLINE=90344224; PubMed=1368518;
RA Montes C., Amador M., Cuevas D., Cordoba F.;
RT "Subunit structure of karatin, the proteinase isolated from
RT Bromelia plumieri (karatas)."
RL Agric. Biol. Chem. 54:17-24(1990).
CC -!- SUBUNIT: Dimer of two small subunits linked by disulfide bonds.
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR PIR; PT0029; PT0029.
DR InterPro; IPR000169; SHprot acsite.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1602 MW; FDA156893F0834FA CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 1 VPETW 5

RESULT 43
MCRX_METTM STANDARD; PRT; 14 AA.
AC P58815;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.-.-) (MCR II

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DE alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91093370; PubMed=22693306;
RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
Methanobacterium thermoautotrophicum strain Marburg and delta H.";
RL Eur. J. Biochem. 194;871-877(1990).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
CC Coenzyme F430 is a yellow nickel porphyrinoid.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1718 MW; D317CCC562F00E29 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FITTVK 7
| : :|
Db 7 FLKALK 12

RESULT 44
SMS1_MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
OS Oncorhynchus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M.scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
prosomatostatins I and II isolated from the pancreatic islets of two
species of teleostean fish: the daddy sculpin and the flounder.";
RL Eur. J. Biochem. 168:647-652(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=O.kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plisetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorbman A.;
RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
somatostatins.";
RL Gen. Comp. Endocrinol. 63:252-263(1986).
RN [3]
RP SEQUENCE.

RC SPECIES=A.anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
structural features from the European eel (Anguilla anguilla).";
RL Gen. Comp. Endocrinol. 72:181-189(1988).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR; A60840; A60840.
DR PIR; B60842; B60842.
DR PIR; S00172; S00172.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Hormone; Multigene family.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FFITT 5
|||
Db 6 FFWKT 10

RESULT 45
SMS_ALLMI STANDARD; PRT; 14 AA.
ID SMS_ALLMI STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496, 34903;
RN [1]
RP SEQUENCE.
RC SPECIES=A.mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
and stomach of the alligator.";
RL Peptides 14:573-579(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=T.scripta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
somatostatin from the turtle, Pseudemys scripta.";
RL Peptides 11:461-466(1990).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR; C60414; C60414.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Hormone.
FT DISULFID 3 14 BY SIMILARITY.
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FFITT 5
|||
Db 6 FFWKT 10

Search completed: August 30, 2004, 10:50:25
Job time : 3.72297 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.00676 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFTVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	21	38.2	13	2 B56864	dipeptidyl-peptida
2	20	36.4	9	2 I46016	cytochrome-c oxida
3	18	32.7	12	2 I77529	estrogen receptor
4	18	32.7	13	2 A59491	epithelial dog all
5	18	32.7	14	2 PT0259	Ig heavy chain CRD
6	18	32.7	14	2 PH1347	Ig heavy chain DJ
7	17	30.9	8	2 A59028	MHC class I histoc
8	17	30.9	11	2 S54347	tubulin beta chain
9	17	30.9	11	2 A49037	Tcr gamma V-J regi
10	17	30.9	11	2 B49037	Tcr gamma V-J regi
11	17	30.9	11	2 C49037	Tcr gamma V-J regi
12	17	30.9	12	2 I64829	gene HEXA protein
13	17	30.9	12	2 PH1675	Ig heavy chain V r
14	17	30.9	13	2 PH1676	Ig heavy chain V r
15	17	30.9	13	2 S70723	lipamide dehydrog
16	17	30.9	14	2 PH1677	Ig heavy chain V r
17	17	30.9	14	2 PH1705	Ig heavy chain V r
18	17	30.9	14	2 S62374	alpha-1-antichymot
19	17	30.9	14	2 PH1625	Ig H chain V-D-J r
20	16	29.1	8	2 A28004	adipokinetic hormo
21	16	29.1	9	2 A24244	adipokinetic hormo
22	16	29.1	9	2 A61357	phyllocaerulein -
23	16	29.1	9	2 A43848	cell surface adhes
24	16	29.1	10	2 A31571	hypertrehalosemic/
25	16	29.1	10	2 A61337	caerulein - frog (
26	16	29.1	12	1 A53709	alpha-conotoxin Im
27	16	29.1	13	2 PC2369	unidentified 85K p
28	16	29.1	13	2 B19434	probable sex-speci
29	16	29.1	14	2 PH1627	Ig H chain V-D-J r

30 15 27.3 9 1 AKLQIM locustamyo-inhibiti
31 15 27.3 9 2 C57444 neuropeptide Grb-A
32 15 27.3 9 2 D57444 neuropeptide Grb-A
33 15 27.3 9 2 A28924 fructose-bisphosph
34 15 27.3 9 2 PT0634 T-cell receptor be
35 15 27.3 10 1 SPPGNK neuromedin K - pig
36 15 27.3 10 2 S66248 processing enzyme,
37 15 27.3 10 2 A27617 triose-phosphate i
38 15 27.3 10 2 PN0165 triose-phosphate i
39 15 27.3 10 2 A35556 hypothetical prote
40 15 27.3 10 2 T13838 cytochrome-c oxida
41 15 27.3 10 2 T13976 cytochrome-c oxida
42 15 27.3 10 2 T17057 cytochrome-c oxida
43 15 27.3 10 2 T12303 cytochrome-c oxida
44 15 27.3 10 2 T14019 cytochrome-c oxida
45 15 27.3 10 2 T17060 cytochrome-c oxida

ALIGNMENTS

RESULT 1
B56864
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: B56864

R;Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993
A;Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border mem
A;Reference number: A56864; MUID:93136203; PMID:8093665
A;Accession: B56864
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <PLA>
A;Experimental source: renal brush-border membrane vesicles
C;Keywords: dipeptidylpeptide hydrolase

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 1 MKTPW 5

RESULT 2
I46016
cytochrome-c oxida (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C;Accession: I46016
R;Blessing, M.; Jorcano, J.L.; Franke, W.W.
EMBO J. 8, 117-126, 1989
A;Title: Enhancer elements directing cell-type-specific expression of cytokeratin genes
A;Reference number: I46016; MUID:89231609; PMID:2469572
A;Accession: I46016
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-9 <BLE>
A;Cross-references: EMBL:X14478; NID:g303; PIDN:CAA32640.1; PID:g577897

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTVKT 8
Db 5 STVKT 9

RESULT 3

I77529
estrogen receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C;Accession: I77529
R;Wang, Y.; Miksicek, R.J.
Mol. Endocrinol. 5, 1707-1715, 1991
A;Title: Identification of a dominant negative form of the human estrogen receptor.
A;Reference number: I57707; MUID:92140401; PMID:1779972
A;Accession: I77529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S79911; NID:g244433; PIDN:AAB21301.1; PID:g244434
C;Keywords: steroid hormone receptor

Query Match 32.7%; Score 18; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
:|:|
Db 2 SVTKAW 7

RESULT 4
A59491
epithelial dog allergen - Canis familiaris (fragment)
C;Species: Canis familiaris
C;Date: 27-Oct-2003 #sequence_revision 27-Oct-2003 #text_change 27-Oct-2003
C;Accession: A59491
R;Saarelainen, S.; Taivainen, A.; RytKM-vnen-Nissinen, M.; Auriola, S.; Immonen, A.; MM-
submitted to the Protein Sequence Database, October 2003
A;Description: Diagnosis of dog allergy with recombinant allergens.
A;Reference number: A59491
A;Accession: A59491
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <VIR>
A;Note: IGE-binding protein; allergen

Query Match 32.7%; Score 18; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
:|:|
Db 5 LTQVSGPW 12

RESULT 5
PT0259
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0259
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0259
A;Molecule type: DNA
A;Residues: 1-14 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 32.7%; Score 18; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKTA 9
:|:|
Db 3 LTTIAA 9

RESULT 6
PH1347
Ig heavy chain DJ region (clone C100-103A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1347
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1347
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 32.7%; Score 18; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITT 5
:|:|
Db 6 FLTT 9

RESULT 7
A59028
MHC class I histocompatibility antigen HLA-C alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001
C;Accession: A59028
R;Escalano, J.M.
submitted to the Protein Sequence Database, August 1998
A;Reference number: A59028
A;Accession: A59028
A;Molecule type: protein
A;Residues: 1-8 <ESC>
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTV 6
:|:|
Db 1 YFYTAV 6

RESULT 8
S54347
tubulin beta chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C;Accession: S54347
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
A;Reference number: S54343; MUID:95194333; PMID:7887910
A;Accession: S54347
A;Molecule type: protein
A;Residues: 1-11 <OKA>

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVK 7
:|:|
Db 7 IATIK 11

RESULT 9

A49037
TCR gamma V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A;Reference number: A49037; MUID:92164730; PMID:1311262
A;Accession: A49037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <EQZ>
A;Cross-references: GB:S90637; NID:g246288; PIDN:AAB21547.1; PID:g246289
A;Experimental source: dendritic epidermal T-cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:90637, NCBIP:90641)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 8 TSW 10

RESULT 10
B49037
TCR gamma V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A;Reference number: A49037; MUID:92164730; PMID:1311262
A;Accession: B49037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <EQZ>
A;Cross-references: GB:S90638; NID:g246290; PIDN:AAB21548.1; PID:g246291
A;Experimental source: dendritic epidermal T-cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:90638, NCBIP:90644)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 8 TSW 10

RESULT 11
C49037
TCR gamma V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: C49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A;Reference number: A49037; MUID:92164730; PMID:1311262
A;Accession: C49037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <EQZ>
A;Cross-references: GB:S90639; NID:g246292; PIDN:AAB21549.1; PID:g246293
A;Experimental source: dendritic epidermal T-cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:90639, NCBIP:90645)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 8 TSW 10

RESULT 12
I64829
gene HEXA protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I64829
R;Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A;Reference number: I51882; MUID:95193801; PMID:7887427
A;Accession: I64829
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S76984; NID:g912781; PIDN:AAD14243.1; PID:g4261943
C;Genetics:
C;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 10.0%; Pred. No. 3.9e+03;
Matches 1; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 FFITTVKTAW 10
:::
Db 2 WYLNKRISILW 11

RESULT 13
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1675
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1675
A;Molecule type: mRNA
A;Residues: 1-12 <MCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 2 TSW 4

RESULT 14
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1676
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 8 TSW 10

RESULT 12
I64829
gene HEXA protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I64829
R;Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A;Reference number: I51882; MUID:95193801; PMID:7887427
A;Accession: I64829
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S76984; NID:g912781; PIDN:AAD14243.1; PID:g4261943
C;Genetics:
C;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 10.0%; Pred. No. 3.9e+03;
Matches 1; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 FFITTVKTAW 10
:::
Db 2 WYLNKRISILW 11

RESULT 13
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1675
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1675
A;Molecule type: mRNA
A;Residues: 1-12 <MCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 2 TSW 4

RESULT 14
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1676
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385

A;Accession: PH1676
A;Molecule type: mRNA
A;Residues: 1-13 <MCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 2 TSW 4

RESULT 15

S70723
lipamide dehydrogenase homolog - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70723
R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.
Mol. Microbiol. 17, 523-531, 1995
A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophil
A;Reference number: S70719; MUID:96100451; PMID:8559071
A;Accession: S70723
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <QIS>
A;Experimental source: strain SL1344

Query Match 30.9%; Score 17; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTVKT 8
|:|
Db 2 TEIKT 6

RESULT 16

PH1677
Ig heavy chain V region (clone NP-6-6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1677
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385

A;Accession: PH1677
A;Molecule type: mRNA
A;Residues: 1-14 <MCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 2 TSW 4

RESULT 17

PH1705
Ig heavy chain V region (clone ASC-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1705
adipokinetic hormone G - two-spotted cricket

R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1705
A;Molecule type: mRNA
A;Residues: 1-14 <MCH>
A;Experimental source: B cell
A;Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 12
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10
|:|
Db 2 TSW 4

RESULT 18

S62374
alpha-1-antichymotrypsin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
C;Accession: S62374
R;Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
Eur. J. Biochem. 235, 821-827, 1996
A;Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin variant
A;Reference number: S62374; MUID:96184564; PMID:8654434
A;Accession: S62374
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14 <TSU>

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFITTV 6
|:|
Db 3 FFMSKV 8

RESULT 19

PH1625
Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1625
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1625
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKT 8
|:|
Db 5 ITTRET 10

RESULT 20

A28004
adipokinetic hormone G - two-spotted cricket

N;Alternate names: AKH-G
 C;Species: Gryllus bimaculatus (two-spotted cricket)
 C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
 C;Accession: A28004
 R;Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
 A;Reference number: A28004; MUID:88106553; PMID:3426616
 A;Accession: A28004
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 | |
 Db 6 TGW 8

RESULT 21
 A24244
 adipokinetic hormone - bollworm
 N;Alternate names: Hez-AKH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C;Accession: A24244
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio
 A;Reference number: A24244; MUID:86186794; PMID:3964263
 A;Accession: A24244
 A;Molecule type: protein
 A;Residues: 1-9 <JAF>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
 | : |
 Db 3 TPTSSW 8

RESULT 22
 A61357
 phyllocaerulein - Sauvage's leaf frog
 C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
 C;Accession: A61357
 R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
 Br. J. Pharmacol. 37, 198-206, 1969
 A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona
 A;Reference number: A61357; MUID:70005484; PMID:5824931
 A;Accession: A61357
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <ANA>
 C;Superfamily: gastrin
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Binding site: sulfate (Tyr) (covalent) #status experimental
 F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 | |
 Db 4 TGW 6

RESULT 23

A43848
 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
 C;Species: Staphylococcus aureus
 C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
 C;Accession: A43848
 R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect. Immun. 60, 899-906, 1992
 A;Title: Binding of heparan sulfate to Staphylococcus aureus.
 A;Reference number: A43848; MUID:92176005; PMID:1541563
 A;Accession: A43848
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <LIA>
 A;Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 | |
 Db 3 TGW 5

RESULT 24

A31571
 hypertrehalosemic/adipokinetic hormone - bollworm
 N;Alternate names: Hez-HrTH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C;Accession: A31571
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
 Biochem. Biophys. Res. Commun. 155, 344-350, 1988
 A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit
 A;Reference number: A31571; MUID:88326324; PMID:3415690
 A;Accession: A31571
 A;Molecule type: protein
 A;Residues: 1-10 <JAF>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 5e+03;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
 | : |
 Db 3 TPTSSW 8

RESULT 25

A61337
 caerulein - frog (Hyla caerulea)
 C;Species: Hyla caerulea
 C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C;Accession: A61337
 R;Anastasi, A.; Erspamer, V.; Endean, R.
 Arch. Biochem. Biophys. 125, 57-68, 1968
 A;Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the sh
 A;Reference number: A61337; MUID:68238534; PMID:5649531

A;Accession: A61337
A;Molecule type: protein
A;Residues: 1-10 <ANA>
C;Comment: The last five amino acids and the carboxyl terminal amide group of this neuro
C;Comment: This amphibian skin peptide can cause a sustained lowering of blood pressure
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
| |
Db 5 TGV 7

RESULT 26
A53709
alpha-conotoxin ImI - cone shell (Conus imperialis)
N;Alternate names: alpha-CTX-ImI
C;Species: Conus imperialis (imperial cone)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53709
R;McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; Oliv
J. Biol. Chem. 269, 16733-16739, 1994
A;Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conotoxi
A;Reference number: A53709; MUID:94266889; PMID:8206995
A;Accession: A53709
A;Molecule type: protein
A;Residues: 1-12 <MCI>
A;Note: Structure confirmed by chemical synthesis
C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F;2-8,3-12/Disulfide bonds: #status experimental
F;12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
: | |
Db 7 RCAW 10

RESULT 27
PC2369
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C;Species: Bacillus cereus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC2369
R;Matsumo, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulation i
A;Reference number: PC2369; MUID:95218265; PMID:7766022
A;Accession: PC2369
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <MAS>

Query Match 29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.6e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
| : |
Db 5 TTENPW 10

RESULT 28

B19434
probable sex-specific protein 2 - Elaphe radiata
C;Species: Elaphe radiata
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1993
C;Accession: B19434
R;Epplen, J.T.; McCarrey, J.R.; Sutou, S.; Ohno, S.
Proc. Natl. Acad. Sci. U.S.A. 79, 3798-3802, 1982
A;Title: Base sequence of a cloned snake W-chromosome DNA fragment and identification of
A;Reference number: A19434; MUID:82247938; PMID:6954524
A;Accession: B19434
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <EPP>

Query Match 29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FITTV 6
| | |
Db 5 FIVTL 9

RESULT 29

PH1627
Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1627
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1627
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 29.1%; Score 16; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKT 8
: | | : |
Db 5 VTTRET 10

RESULT 30

AKLQIM
locustamyoinhibiting peptide - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: A60065
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI
A;Reference number: A60065; MUID:92179466; PMID:1796179
A;Accession: A60065
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and
C;Superfamily: locustamyoinhibiting peptide
C;Keywords: amidated carboxyl end; hormone
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10

Db ||
 1 AW 2

RESULT 31

C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: C57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
 ||
 1 AW 2

RESULT 32

D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
 ||
 1 AW 2

RESULT 33

A28924
fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 07-Feb-1997
C;Accession: A28924
R;Lacko, A.G.; Brox, L.W.; Gracy, R.W.; Horecker, B.L.
J. Biol. Chem. 245, 2140-2141, 1970
A;Title: The carboxyl-terminal structure of rabbit liver aldolase (aldolase B).
A;Reference number: A28924; MUID:70166720; PMID:5440846
A;Accession: A28924
A;Molecule type: protein
A;Residues: 1-9 <LAK>
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; pen

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITT 5
 | ||

Db 2 FLATT 6

RESULT 34

PT0634
T-cell receptor beta chain V-D-J region (121-2CL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0634
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0634
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-9 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
 ||
 5 AW 6

RESULT 35

SPPGNK
neuromedin K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
C;Accession: A01560
R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
A;Reference number: A01560; MUID:83282812; PMID:6576785
A;Accession: A01560
A;Molecule type: protein
A;Residues: 1-10 <KAN>
A;Note: the structure of the peptide was confirmed by synthesis
C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth mus
C;Superfamily: neurokinin B precursor
C;Keywords: amidated carboxyl end; hormone; spinal cord
F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
 ||
 5 FFV 7

RESULT 36

S66248
processing enzyme, 33K - black gram (fragment)
C;Species: Vigna mungo (black gram)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S66248
R;Okamoto, T.; Minamikawa, T.
Eur. J. Biochem. 231, 300-305, 1995
A;Title: Purification of a processing enzyme (VmPE-1) that is involved in post-translatic
A;Reference number: S66248; MUID:95361851; PMID:7635141
A;Accession: S66248
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <OKA>

Query Match 27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
||
Db 4 TRW 6

RESULT 37
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C;Species: Nicotiana glauca (curled-leaved tobacco)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C;Accession: A27617
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A;Reference number: A94167
A;Accession: A27617
A;Molecule type: protein
A;Residues: 1-10 <BAU>
C;Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pentose

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
||
Db 4 FFV 6

RESULT 38
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi-
A;Reference number: PN0160
A;Accession: PN0165
A;Molecule type: protein
A;Residues: 1-10 <FUK>
A;Experimental source: strain M-1-1
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
||
Db 4 FFV 6

RESULT 39
A35556
hypothetical protein (ODC region) - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C;Accession: A35556
R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D.
J. Biol. Chem. 265, 4884-4892, 1990
A;Title: Isolation and expression of a human ornithine decarboxylase gene.
A;Reference number: A35556; MUID:90202959; PMID:2318872
A;Accession: A35556
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <MOS>
A;Cross-references: GB:J05271

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
||
Db 7 AW 8

RESULT 40
T13838
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
C;Species: mitochondrion Bipes biporus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13838
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T13838
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71335; NID:gl753232; PID:gl753235; PIDN:AAB48271.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFT 4
||
Db 7 FFT 10

RESULT 41
T13976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment)
C;Species: mitochondrion Cnemidophorus tigris
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13976
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T13976
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U71332; NID:gl753236; PID:gl753239; PIDN:AAB48274.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFT 4
||
Db 7 FFT 10

RESULT 42
T17057
cytochrome-c oxidase (EC 1.9.3.1) chain I - Crotaphytus collaris mitochondrion (fragment)
C;Species: mitochondrion Crotaphytus collaris
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17057

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17057

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U82681; NID:g3603108; PID:g3603111; PIDN:AAC62272.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 27.3%; Score 15; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFIT 4

Db 7 FFST 10

RESULT 43

T12303

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Dipsosaurus dorsalis mitochondrion (fragment

C;Species: mitochondrion Dipsosaurus dorsalis

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999

C;Accession: T12303

R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi

A;Reference number: Z17488; MUID:99162288; PMID:10051389

A;Accession: T12303

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <SCH>

A;Cross-references: EMBL:AF049857; NID:g4105726; PID:g4105729; PIDN:AAD02514.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 27.3%; Score 15; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFIT 4

Db 7 FFST 10

RESULT 44

T14019

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Eremias grammica mitochondrion (fragment)

C;Species: mitochondrion Eremias grammica

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C;Accession: T14019

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A;Title: Two novel gene orders and the role of light-strand replication in rearrangement

A;Reference number: Z17789; MUID:97153826; PMID:9000757

A;Accession: T14019

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U71331; NID:gl753240; PID:gl753243; PIDN:AAB48277.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match

27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFIT 4

Db 7 FFST 10

RESULT 45

T17060

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Gambelia wislizenii mitochondrion (fragment)

C;Species: mitochondrion Gambelia wislizenii

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C;Accession: T17060

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17060

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U82682; NID:g3603120; PID:g3603123; PIDN:AAC62281.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 27.3%; Score 15; DB 2; Length 10;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFIT 4

Db 7 FFST 10

Search completed: August 30, 2004, 10:58:53

Job time : 4.00676 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 12.2297 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	54.5	13	10	US-09-991-225-19
2	30	54.5	13	10	US-09-991-225-38
3	30	54.5	13	12	US-10-369-405-19
4	30	54.5	13	12	US-10-369-405-38
5	27	49.1	13	14	US-10-174-105A-184
6	25	45.5	9	10	US-09-932-165-452
7	25	45.5	9	10	US-09-932-165-660
8	25	45.5	9	10	US-09-932-165-872
9	25	45.5	10	10	US-09-932-165-558
10	25	45.5	10	10	US-09-932-165-751
11	25	45.5	10	10	US-09-932-165-1369
12	25	45.5	10	10	US-09-932-165-1372
13	25	45.5	10	12	US-10-601-837-88
14	25	45.5	10	16	US-10-432-234A-31
15	25	45.5	10	16	US-10-432-234A-32

16	25	45.5	12	14	US-10-286-457-425	Sequence 425, App
17	24	43.6	8	14	US-10-224-999A-126	Sequence 126, App
18	24	43.6	9	14	US-10-224-999A-131	Sequence 131, App
19	24	43.6	9	14	US-10-224-999A-132	Sequence 132, App
20	24	43.6	10	14	US-10-224-999A-137	Sequence 137, App
21	24	43.6	10	14	US-10-224-999A-138	Sequence 138, App
22	24	43.6	10	14	US-10-224-999A-139	Sequence 139, App
23	24	43.6	11	14	US-10-224-999A-144	Sequence 144, App
24	24	43.6	11	14	US-10-224-999A-145	Sequence 145, App
25	24	43.6	11	14	US-10-224-999A-146	Sequence 146, App
26	24	43.6	11	14	US-10-224-999A-147	Sequence 147, App
27	24	43.6	12	14	US-10-224-999A-152	Sequence 152, App
28	24	43.6	12	14	US-10-224-999A-153	Sequence 153, App
29	24	43.6	12	14	US-10-224-999A-154	Sequence 154, App
30	24	43.6	12	14	US-10-224-999A-155	Sequence 155, App
31	24	43.6	12	14	US-10-224-999A-156	Sequence 156, App
32	24	43.6	12	16	US-10-203-969A-235	Sequence 235, App
33	24	43.6	12	16	US-10-203-969A-236	Sequence 236, App
34	24	43.6	12	16	US-10-203-969A-237	Sequence 237, App
35	24	43.6	12	16	US-10-203-969A-238	Sequence 238, App
36	24	43.6	12	16	US-10-203-969A-418	Sequence 418, App
37	24	43.6	12	16	US-10-203-969A-419	Sequence 419, App
38	24	43.6	12	16	US-10-203-969A-420	Sequence 420, App
39	24	43.6	12	16	US-10-642-553-102	Sequence 102, App
40	24	43.6	12	16	US-10-642-553-103	Sequence 103, App
41	24	43.6	12	16	US-10-642-553-104	Sequence 104, App
42	24	43.6	12	16	US-10-642-553-105	Sequence 105, App
43	24	43.6	12	16	US-10-642-553-275	Sequence 275, App
44	24	43.6	13	14	US-10-219-834-95	Sequence 95, Appl
45	24	43.6	13	14	US-10-224-999A-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-09-991-225-19
; Sequence 19, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY11, EXPRESSED HIG
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-991-225-19

Query Match 54.5%; Score 30; DB 10; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ITTVKTAW 10
:|:|:|:
Db 4 VTSIRSAW 11

RESULT 2
US-09-991-225-38
; Sequence 38, Application US/09991225
; Publication No. US20030153063A1

```
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-991-225-38
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```
Query Match 54.5%; Score 30; DB 10; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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QY 3 ITTVKTAW 10
:|:::|
Db 4 VTSIRSAW 11
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RESULT 3
US-10-369-405-19
; Sequence 19, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS
; FILE REFERENCE: D0075A CIP
; CURRENT APPLICATION NUMBER: US/10/369,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-369-405-19
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```
Query Match 54.5%; Score 30; DB 12; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 ITTVKTAW 10
:|:::|
Db 4 VTSIRSAW 11
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RESULT 4
US-10-369-405-38
; Sequence 38, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS
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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0075A CIP
; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-369-405-38
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Query Match 54.5%; Score 30; DB 12; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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QY 3 ITTVKTAW 10
:|:::|
Db 4 VTSIRSAW 11
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RESULT 5
US-10-174-105A-184
; Sequence 184, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 184
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 5 is phosphorylated
US-10-174-105A-184
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```
Query Match 49.1%; Score 27; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 3 ITTVKTAW 10
:|:::|
Db 3 LATVKSrw 10
```

```
RESULT 6
US-09-932-165-452
; Sequence 452, Application US/09932165
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Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 452
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-452

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 3 FFFTNK 9

RESULT 7
US-09-932-165-660
Sequence 660, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 660
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-660

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 3 FFFTNK 9

QY 1 FFITTVK 7
||| :|
Db 3 FFFTNK 9

RESULT 8
US-09-932-165-872
Sequence 872, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 872
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-872

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 1 FFFTNK 7

RESULT 9
US-09-932-165-558
Sequence 558, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 558
LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-558

Query Match      45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FFITTVK 7
      ||| | :|
Db      4 FFFFTNIK 10

RESULT 10
US-09-932-165-751
; Sequence 751, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 751
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-751

Query Match      45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FFITTVK 7
      ||| | :|
Db      4 FFFFTNIK 10

RESULT 11
US-09-932-165-1369
; Sequence 1369, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
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; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1369
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1369
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Query Match      45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FFITTVK 7
      ||| | :|
Db      2 FFFFTNIK 8
```

```
RESULT 12
US-09-932-165-1372
; Sequence 1372, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1372
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1372
```

```
Query Match      45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FFITTVK 7
      ||| | :|
Db      1 FFFFTNIK 7
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RESULT 13
US-10-601-837-88
; Sequence 88, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
```

```
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidn
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309A1vegicus
US-10-601-837-88

Query Match      45.5%; Score 25; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FITTVK 7
      |||||
Db      3 FITTVQ 8

RESULT 14
US-10-432-234A-31
; Sequence 31, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Biota Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432,234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-432-234A-31

Query Match      45.5%; Score 25; DB 16; Length 10;
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      ::: :|
Db      2 YLSALRTGW 10

RESULT 15
US-10-432-234A-32
; Sequence 32, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Biota Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432,234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 10
; TYPE: PRT
```

```
; ORGANISM: respiratory syncytial virus
US-10-432-234A-32

Query Match      45.5%; Score 25; DB 16; Length 10;
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      ::: :|
Db      1 YLSALRTGW 9

RESULT 16
US-10-286-457-425
; Sequence 425, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 425
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-425

Query Match      45.5%; Score 25; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 TVKTAW 10
      |||
Db      1 TVKAGW 6

RESULT 17
US-10-224-999A-126
; Sequence 126, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-126

Query Match      43.6%; Score 24; DB 14; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      :|||
```

```
Db          1 LTTVPTA 7

RESULT 18
US-10-224-999A-131
; Sequence 131, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-131

Query Match          43.6%; Score 24; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          3 ITTVKTA 9
           :||| ||
Db          2 LTTVPTA 8

RESULT 19
US-10-224-999A-132
; Sequence 132, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-132

Query Match          43.6%; Score 24; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          3 ITTVKTA 9
           :||| ||
Db          2 LTTVPTA 8

RESULT 20
US-10-224-999A-137
; Sequence 137, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-137

Query Match          43.6%; Score 24; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          3 ITTVKTA 9
           :||| ||
Db          2 LTTVPTA 8

RESULT 21
US-10-224-999A-138
; Sequence 138, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-138

Query Match          43.6%; Score 24; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          3 ITTVKTA 9
           :||| ||
Db          2 LTTVPTA 8

RESULT 22
US-10-224-999A-139
; Sequence 139, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-139

Query Match          43.6%; Score 24; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          3 ITTVKTA 9
           :||| ||
Db          2 LTTVPTA 8
```


; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-139

Query Match 43.6%; Score 24; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
:|||||
Db 1 LTTVPTA 7

RESULT 23

US-10-224-999A-144
; Sequence 144, Application US/10224999A
; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 144

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-144

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
:|||||
Db 4 LTTVPTA 10

RESULT 24

US-10-224-999A-145

; Sequence 145, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 145

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-145

Query Match 43.6%; Score 24; DB 14; Length 11;

Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
:|||||
Db 3 LTTVPTA 9

RESULT 25

US-10-224-999A-146

; Sequence 146, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 146

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-146

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
:|||||
Db 2 LTTVPTA 8

RESULT 26

US-10-224-999A-147

; Sequence 147, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 147

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-147

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
:|||||
Db 1 LTTVPTA 7

RESULT 27

```
US-10-224-999A-152
; Sequence 152, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-152

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      :||| ||
Db      5 LTTVPTA 11

RESULT 28
US-10-224-999A-153
; Sequence 153, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-153

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      :||| ||
Db      4 LTTVPTA 10

RESULT 29
US-10-224-999A-154
; Sequence 154, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
```

```
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-154

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      :||| ||
Db      3 LTTVPTA 9

RESULT 30
US-10-224-999A-155
; Sequence 155, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-155

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      :||| ||
Db      2 LTTVPTA 8

RESULT 31
US-10-224-999A-156
; Sequence 156, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 12
```

```
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-156

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
Db      1 LTTVPTA 7

RESULT 32
US-10-203-969A-235
; Sequence 235, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-235

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
Db      4 FCISINTTW 12

RESULT 33
US-10-203-969A-236
; Sequence 236, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-237

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
Db      2 FCISINTTW 10

RESULT 34
US-10-203-969A-237
; Sequence 237, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-237

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
Db      2 FCISINTTW 10

RESULT 35
US-10-203-969A-238
; Sequence 238, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 238
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-238
```

```
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 238
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-238

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      |::||
Db      1 FCISINTTW 9

RESULT 36
US-10-203-969A-418
; Sequence 418, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 418
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide
; OTHER INFORMATION: derived from hFSH with an additional C- or N-
; OTHER INFORMATION: terminal cysteine
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-418

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      |::||
Db      3 FCISINTTW 11

RESULT 37
US-10-203-969A-419
; Sequence 419, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
```

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; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 419
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide
; OTHER INFORMATION: derived from hFSH with an additional C- or N-
; OTHER INFORMATION: terminal cysteine
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-419

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      |::||
Db      3 FCISINTTW 11

RESULT 38
US-10-203-969A-420
; Sequence 420, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Dijk van, Evert
; APPLICANT: Slootstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT APPLICATION NUMBER: US/10/203,969A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 420
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide
; OTHER INFORMATION: derived from hFSH with an additional C- or N-
; OTHER INFORMATION: terminal cysteine
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-420

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
      |::||
Db      1 FCISINTTW 9

RESULT 39
US-10-642-553-102
; Sequence 102, Application US/10642553
```

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; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-102

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
DB      4 FCISINTW 12

RESULT 40
US-10-642-553-103
; Sequence 103, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-103

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
DB      3 FCISINTW 11

RESULT 41
US-10-642-553-104
; Sequence 104, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
```

```
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-104

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
DB      2 FCISINTW 10

RESULT 42
US-10-642-553-105
; Sequence 105, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-105

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FITTVKTAW 10
DB      1 FCISINTW 9

RESULT 43
US-10-642-553-275
; Sequence 275, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fragment of hFSH with Cys attached to the C or N terminal
US-10-642-553-275

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FTTTVKTAW 10
      | : : |
Db      1 FCISINTTW 9

RESULT 44
US-10-219-834-95
; Sequence 95, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-95

Query Match      43.6%; Score 24; DB 14; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 FFTTVKTAW 10
      || : : |
Db      2 FFVGSFRKQW 11

RESULT 45
US-10-224-999A-161
; Sequence 161, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-161

Query Match      43.6%; Score 24; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ITTVKTA 9
      : ||| |
Db      6 LTTVPTA 12

Search completed: August 30, 2004, 11:05:01
Job time : 13.2297 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.9527 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	52.7	14	2	US-08-609-271-7
2	29	52.7	14	3	US-08-188-374-7
3	23	41.8	12	2	US-08-637-759B-97
4	23	41.8	12	3	US-08-871-355A-97
5	23	41.8	12	3	US-08-912-560-9
6	23	41.8	12	4	US-09-201-945-97
7	22	40.0	8	3	US-08-467-472C-5
8	22	40.0	8	3	US-08-467-472C-6
9	22	40.0	8	3	US-09-384-061-5
10	22	40.0	8	3	US-09-384-061-6
11	22	40.0	8	4	US-09-852-870A-5
12	22	40.0	10	2	US-08-704-655-20
13	22	40.0	10	4	US-08-852-870A-6
14	22	40.0	11	2	US-08-727-688-24
15	22	40.0	11	3	US-09-113-977C-9
16	22	40.0	11	4	US-09-351-048A-9
17	22	40.0	11	4	US-09-069-827A-42
18	22	40.0	12	4	US-09-832-161-27
19	22	40.0	13	6	5496924-54
20	22	40.0	14	6	5496924-48
21	21	38.2	8	1	US-08-233-558-20
22	21	38.2	8	3	US-08-405-647B-15
23	21	38.2	8	3	US-09-074-658-52
24	21	38.2	8	3	US-08-985-499-15
25	21	38.2	8	5	PCT-US96-03180-15
26	21	38.2	8	6	5514646-27
27	21	38.2	9	1	US-08-425-238-6

28	21	38.2	9	1	US-08-425-238-10	Sequence 10, Appl
29	21	38.2	9	2	US-08-717-169-18	Sequence 18, Appl
30	21	38.2	9	2	US-08-867-941-52	Sequence 52, Appl
31	21	38.2	9	2	US-08-286-861-12	Sequence 12, Appl
32	21	38.2	9	4	US-09-424-656-13	Sequence 13, Appl
33	21	38.2	9	4	US-09-228-901A-18	Sequence 18, Appl
34	21	38.2	10	4	US-09-490-702B-89	Sequence 89, Appl
35	21	38.2	12	4	US-09-424-656-11	Sequence 11, Appl
36	21	38.2	12	4	US-09-424-656-12	Sequence 12, Appl
37	21	38.2	12	6	5489533-16	Patent No. 5489533
38	21	38.2	12	6	5512660-16	Patent No. 5512660
39	21	38.2	13	1	US-08-425-238-3	Sequence 3, Appli
40	21	38.2	13	1	US-08-425-238-11	Sequence 11, Appl
41	21	38.2	13	2	US-08-701-124-35	Sequence 35, Appl
42	21	38.2	13	2	US-08-286-861-6	Sequence 6, Appli
43	21	38.2	13	3	US-09-130-225-35	Sequence 35, Appl
44	21	38.2	13	3	US-09-177-249-199	Sequence 199, App
45	21	38.2	13	4	US-09-406-781-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-08-609-271-7
; Sequence 7, Application US/08609271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Site FD-1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,271
; FILING DATE: 28 February 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,374
; FILING DATE: 1/27/94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5811264elli, Marianne F.
; REGISTRATION NUMBER: 38571
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32547
; REFERENCE/DOCKET NUMBER: 170/Div
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
US-08-609-271-7

Query Match 52.7%; Score 29; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 55;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 TTVKTAW 10
| | | |
Db 8 TNVKAAM 14

RESULT 2
US-08-188-374-7
; Sequence 7, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth
; FILE REFERENCE: EXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide from
; OTHER INFORMATION: horse, donkey, kulan, zebra or gundi
US-08-188-374-7

Query Match 52.7%; Score 29; DB 3; Length 14;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
| | | |
Db 8 TNVKAAM 14

RESULT 3
US-08-637-759B-97
; Sequence 97, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-97

Query Match 41.8%; Score 23; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
| | | |
Db 1 TVNTHW 6

RESULT 4
US-08-871-355A-97
; Sequence 97, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-97

Query Match 41.8%; Score 23; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10

```
Db          ||| | |
            1 TVNTHW 6

RESULT 5
US-08-912-560-9
; Sequence 9, Application US/08912560A
; Patent No. 6066484
; GENERAL INFORMATION:
; APPLICANT: HATANAKA, Haruyo
; APPLICANT: ASHIKARI, Toshihiko
; APPLICANT: OGAWA, Jun
; APPLICANT: SHIMIZU, Sakayu
; TITLE OF INVENTION: NOVEL PURINE NUCLEOSIDASE
; FILE REFERENCE: 001560-309
; CURRENT APPLICATION NUMBER: US/08/912,560A
; CURRENT FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: JP 8-216421
; EARLIER FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Ochrobactrum anthropi
US-08-912-560-9

Query Match          41.8%; Score 23; DB 3; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY          1 FFIITVK 7
            | : |||
Db          6 FIVNTVK 12

RESULT 6
US-09-201-945-97
; Sequence 97, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 97:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-97

Query Match          41.8%; Score 23; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          5 TVKTAW 10
            ||| | |
Db          1 TVNTHW 6

RESULT 7
US-08-467-472C-5
; Sequence 5, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
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; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-08-467-472C-5
;
; Query Match 40.0%; Score 22; DB 3; Length 8;
; Best Local Similarity 75.0%; Pred. No. 3e+05;
; Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
QY 7 KTAW 10
Db ||:|
5 KTSW 8
;
; RESULT 8
; US-08-467-472C-6
; Sequence 6, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
```

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; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
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PUBLICATION DATE: 40.0%; Score 22; DB 3; Length 8;
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-6

Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
||:|
Db 5 KTSW 8

RESULT 9

US-09-384-061-5
Sequence 5, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HADT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR

MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-5

Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
||:|
Db 5 KTSW 8

RESULT 10
US-09-384-061-6
; Sequence 6, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; POSITION IN GENOME: N/A.
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:

; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-6
Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 KTAW 10
Db 5 KTSW 8
RESULT 11
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-5
Query Match 40.0%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 KTAW 10
||:|

```
Db          5 KTSW 8

RESULT 12
US-08-704-655-20
; Sequence 20, Application US/08704655
; Patent No. 5869453
; GENERAL INFORMATION:
; APPLICANT: Moss, Denis J.
; APPLICANT: Burrows, Scott R.
; APPLICANT: Khanna, Rajiv
; APPLICANT: Kerr, Veberly M.
; APPLICANT: Burrows, Jacqueline M.
; APPLICANT: Subbier, Andreas
; TITLE OF INVENTION: Cytotoxic T Cell Epitopes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,655
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU95/00140
; FILING DATE: 16-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (712) 789-2679
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-704-655-20

Query Match          40.0%; Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY          3 ITTVKTAW 10
Db          3 ITPYKPTW 10

RESULT 13
US-09-852-870A-6
; Sequence 6, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24

Query Match          40.0%; Score 22; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          6 VKTAW 10
Db          2 METAW 6

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
; NAME/KEY: SITE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Xaa= D-Phe, D-beta-Nal, or Phe
US-09-852-870A-6

Query Match          40.0%; Score 22; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          7 KTAW 10
Db          7 KTSW 10

RESULT 14
US-08-727-688-24
; Sequence 24, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
US-08-727-688-24

Query Match          40.0%; Score 22; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY          6 VKTAW 10
Db          2 METAW 6
```

RESULT 15
US-09-113-977C-9
; Sequence 9, Application US/09113977C
; Patent No. 6277824
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; TITLE OF INVENTION: FUNCTION
; FILE REFERENCE: 100086.403
; CURRENT APPLICATION NUMBER: US/09/113,977C
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
; NAME/KEY: MOD RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: Residue may be native or modified
; NAME/KEY: MOD RES
; LOCATION: (11)...(11)
; OTHER INFORMATION: Residue may be native or modified
US-09-113-977C-9

Query Match 40.0%; Score 22; DB 3; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FITTVKTAW 10
|| :||
Db 2 FIIRRTGW 10

RESULT 16
US-09-351-048A-9
; Sequence 9, Application US/09351048A
; Patent No. 6472368
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; TITLE OF INVENTION: FUNCTION
; FILE REFERENCE: 100086.403C1
; CURRENT APPLICATION NUMBER: US/09/351,048A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-351-048A-9

Query Match 40.0%; Score 22; DB 4; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FITTVKTAW 10
|| :||
Db 2 FIIRRTGW 10

RESULT 17
US-09-069-827A-42
; Sequence 42, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M
; APPLICANT: KAY, Brian K
; APPLICANT: FRELINGER, Jeffrey A
; APPLICANT: HYDE-DERUYSCHE, Robin P
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
; TITLE OF INVENTION: COMPLEMENTARY COMBINATORIAL LIBRARIES
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-069-827A-42

Query Match 40.0%; Score 22; DB 4; Length 11;
Best Local Similarity 37.5%; Pred. No. 7.2e+02;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ITTVKTAW 10
: : :
Db 2 VPTTKVLW 9

RESULT 18
US-09-832-161-27
; Sequence 27, Application US/09832161
; Patent No. 6656713
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris

; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; FILE REFERENCE: NF-KB
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-27

Query Match 40.0%; Score 22; DB 4; Length 12;
Best Local Similarity 37.5%; Pred. No. 7.8e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
| | | | |
Db 4 IETIESNW 11

RESULT 19
5496924-54
; Patent No. 5496924
; APPLICANT: HABERMANN, PAUL; WENGENMAYER, FRIEDRICH
; TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN
; INTERLEUKIN-2 FRAGMENT BALLAST PORTION
; NUMBER OF SEQUENCES: 56
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,545
; FILING DATE: 28-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 377,313
; FILING DATE: 10-JUL-1989
; APPLICATION NUMBER: 934,910
; FILING DATE: 25-NOV-1986
; APPLICATION NUMBER: 943,804
; FILING DATE: 19-DEC-1986
; SEQ ID NO: 54:
; LENGTH: 13
5496924-54

Query Match 40.0%; Score 22; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 8.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| | | | |
Db 2 FMITTYSLA 10

RESULT 20
5496924-48
; Patent No. 5496924
; APPLICANT: HABERMANN, PAUL; WENGENMAYER, FRIEDRICH
; TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN
; INTERLEUKIN-2 FRAGMENT BALLAST PORTION
; NUMBER OF SEQUENCES: 56
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,545
; FILING DATE: 28-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 377,313
; FILING DATE: 10-JUL-1989
; APPLICATION NUMBER: 934,910
; FILING DATE: 25-NOV-1986
; APPLICATION NUMBER: 943,804
; FILING DATE: 19-DEC-1986
; SEQ ID NO: 48:

; LENGTH: 14
5496924-48

Query Match 40.0%; Score 22; DB 6; Length 14;
Best Local Similarity 55.6%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| | | | |
Db 3 FMITTYSLA 11

RESULT 21
US-08-233-558-20
; Sequence 20, Application US/08233558
; Patent No. 5480870
; GENERAL INFORMATION:
; APPLICANT: Keri, Gyorgy
; APPLICANT: Mezo, Imre
; APPLICANT: Horvath, Aniko
; APPLICANT: Vadasz, Zsolt
; APPLICANT: Teplan, Istvan
; APPLICANT: Balogh, Agnes
; APPLICANT: Csuka, Orsolya
; APPLICANT: Bokonyi, Gyongyi
; APPLICANT: Szoke, Balazs
; APPLICANT: Horvath, Judit
; TITLE OF INVENTION: No. 5480870el Tumour Growth-Inhibiting
; TITLE OF INVENTION: Somatostatin Analogues, Pharmaceutical Compositions
; TITLE OF INVENTION: containing them and Process for Preparing Same
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 360 Kb storage
; COMPUTER: IBM AT-compatible, 80286 processor
; OPERATING SYSTEM: MS-DOS version 5.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,558
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/772,808
; FILING DATE: 08-OCT-1991
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-233-558-20

Query Match 38.2%; Score 21; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
| | | | |
Db 5 KTCW 8

RESULT 22
US-08-405-647B-15
; Sequence 15, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.

APPLICANT: Crandall, Ian E.
APPLICANT: Sholet, Stephen B.
APPLICANT: Thevenin, Bernard Jean-Marie
TITLE OF INVENTION: Compositions and Methods for Reducing
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 02307E-068700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-405-647B-15

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKT 8
Db 1 FVKRVKT 7

RESULT 23
US-09-074-658-52
Sequence 52, Application US/09074658
Patent No. 6184371
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658

FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-52

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKT 8
Db 1 MSTVKT 6

RESULT 24
US-08-985-499-15
Sequence 15, Application US/08985499
Patent No. 6191103
GENERAL INFORMATION:
APPLICANT: Shohet, Stephen B.
APPLICANT: Sherman, Irwin
APPLICANT: von Andrian, Ulrich
TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
TITLE OF INVENTION: Mammal
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,499
FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02307E-084500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-985-499-15

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKT 8
|: |||
Db 1 FVKRVKT 7

RESULT 25
PCT-US96-03180-15
; Sequence 15, Application PC/TUS9603180
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03180
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-03180-15

Query Match 38.2%; Score 21; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKT 8
|: |||
Db 1 FVKRVKT 7

RESULT 26
5514646-27
; Patent No. 5514646
; APPLICANT: CHANCE, RONALD E.; DIMARCHI, RICHARD D.; FRANK,
; BRUCE H.; SHIELDS, JAMES E.
; TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; NUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,201
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,632
; FILING DATE: 17-APR-1991
; APPLICATION NUMBER: 388,201
; FILING DATE: 04-AUG-1989
; APPLICATION NUMBER: 308,352
; FILING DATE: 09-FEB-1989
; SEQ ID NO: 27:

; LENGTH: 8
5514646-27

Query Match 38.2%; Score 21; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFITT 5
|: |||
Db 2 FFYTT 6

RESULT 27
US-08-425-238-6
; Sequence 6, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-425-238-6

Query Match 38.2%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
|: |||
Db 4 ETAW 7

RESULT 28
US-08-425-238-10
; Sequence 10, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa = an amino acid capable
; OTHER INFORMATION: of forming a disulfide bond."
;
; NAME/KEY: Peptide
; LOCATION: 9
; OTHER INFORMATION: /note= "Xaa = an amino acid capable
; OTHER INFORMATION: of forming a disulfide bond."
;
US-08-425-238-10

Query Match 38.2%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred.No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 4 ETAW 7

RESULT 29
US-08-717-169-18
; Sequence 18, Application US/08717169
; Patent No. 5922676
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,169
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-717-169-18

Query Match 38.2%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred.No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 4 ETAW 7

RESULT 30
US-08-867-941-52
; Sequence 52, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-867-941-52
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Query Match 38.2%; Score 21; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKT 8
: : : : :
Db 1 MSTVKT 6

RESULT 31
US-08-286-861-12
; Sequence 12, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-286-861-12

Query Match 38.2%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
: : : : :
Db 4 ETAW 7

RESULT 32
US-09-424-656-13
; Sequence 13, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-13

Query Match 38.2%; Score 21; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
: : : : :
Db 4 ETAW 7

RESULT 33
US-09-228-901A-18
; Sequence 18, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer by Using Superfibronectin
; FILE REFERENCE: P-TX 3416
; CURRENT APPLICATION NUMBER: US/09/228,901A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 08/717,169
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-228-901A-18

Query Match 38.2%; Score 21; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
: : : : :
Db 4 ETAW 7

RESULT 34
US-09-490-702B-89
; Sequence 89, Application US/09490702B
; Patent No. 6560542
; GENERAL INFORMATION:
; APPLICANT: Mandell, Arnold
; APPLICANT: Selz, Karen
; APPLICANT: Shlesinger, Michael
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of th
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins
; FILE REFERENCE: 01561-0002-00US00
; CURRENT APPLICATION NUMBER: US/09/490,702B
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: synthetic
US-09-490-702B-89

Query Match      38.2%; Score 21; DB 4; Length 10;
Best Local Similarity 25.0%; Pred. No. 9.8e+02;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 ITTVKTAW 10
Db      1 VQTSSRW 8

RESULT 35
US-09-424-656-11
; Sequence 11, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-11

Query Match      38.2%; Score 21; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 KTAW 10
Db      6 ETAW 9

RESULT 36
US-09-424-656-12
; Sequence 12, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; TITLE OF INVENTION: ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-424-656-12

Query Match      38.2%; Score 21; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 KTAW 10
Db      6 ETAW 9

RESULT 37
5489533-16
; Patent No. 5489533
; APPLICANT: SPRINGER, TIMOTHY A.;STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; ICAM-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,814
; FILING DATE: 06-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,3075
; FILING DATE: 12-JUL-1995
; APPLICATION NUMBER: 89,307
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO:16:
; LENGTH: 12
5489533-16

Query Match      38.2%; Score 21; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 VKTAW 10
Db      6 VRAAW 10

RESULT 38
5512660-16
; Patent No. 5512660
; APPLICANT: SPRINGER, TIMOTHY A.;STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: PURIFIED ICAM-2 AND FRAGMENT THEREOF
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,613
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,307
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;
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO:16:
; LENGTH: 12
5512660-16

Query Match 38.2%; Score 21; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
|: ||
Db 6 VRAAW 10

RESULT 39
US-08-425-238-3
; Sequence 3, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-425-238-3
Query Match 38.2%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
: |||
Db 6 ETAW 9

RESULT 40
US-08-425-238-11
; Sequence 11, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: Peptide
LOCATION: 3
OTHER INFORMATION: /note= "Xaa = an amino acid capable
of forming a disulfide bond."
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
LOCATION: 11
OTHER INFORMATION: /note= "Xaa = an amino acid capable
of forming a disulfide bond."
US-08-425-238-11

Query Match 38.2%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
: |||
Db 6 ETAW 9

RESULT 41
US-08-701-124-35
; Sequence 35, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.

; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-35

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
:||||
Db 6 ETAW 9

RESULT 42
US-08-286-861-6
; Sequence 6, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-286-861-6

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
:||||
Db 6 ETAW 9

RESULT 43
US-09-130-225-35
; Sequence 35, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-225-35

Query Match 38.2%; Score 21; DB 3; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
:||||
Db 6 ETAW 9

RESULT 44
US-09-177-249-199
; Sequence 199, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-199

Query Match 38.2%; Score 21; DB 3; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
|||
Db 1 KTCW 4

RESULT 45
US-09-406-781-63
; Sequence 63, Application US/09406781
; Patent No. 6306663
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-3
; CURRENT APPLICATION NUMBER: US/09/406,781
; CURRENT FILING DATE: 1999-09-28
; EARLIER APPLICATION NUMBER: 60/119,851
; EARLIER FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-406-781-63

Query Match 38.2%; Score 21; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
:|
Db 6 ETAW 9

Search completed: August 30, 2004, 10:57:20
Job time : 5.9527 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 309.892 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 1083

Sequence: 1 MKVLLAAALIAAGSVFFLLP.....VIIADCGKIEVKPFAIAKE 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	83	7.7	14	6	ABP74769 Proteome
2	71	6.6	11	3	AAY69925 Human cys
3	63	5.8	10	3	AAY69947 Human cys
4	63	5.8	10	6	ABR84352 Human cys
5	63	5.8	11	3	AAY69926 Human cys
6	60	5.5	11	3	AAY69924 Human cys
7	58	5.4	9	3	AAY69928 Human cys
8	58	5.4	10	3	AAY69930 Human cys
9	57	5.3	11	3	AAY69944 Human cys
10	55	5.1	10	3	AAY69929 Human cys
11	55	5.1	11	3	AAY69943 Human cys
12	54	5.0	14	5	ABG67616 Human ADP
13	54	5.0	14	6	ADA23735 Alzheimer
14	53	4.9	10	3	AAY69949 Human cys
15	52	4.8	10	3	AAY69945 Human cys
16	51	4.7	9	3	AAY69923 Human cys
17	51	4.7	11	3	AAY69955 Human cys
18	50	4.6	9	3	AAY69922 Human cys
19	50	4.6	9	3	AAY69927 Human cys
20	50	4.6	9	4	AAB46931 Human cys
21	50	4.6	9	4	AAG68089 Antitumou
22	50	4.6	9	5	ABG79076 Human cys
23	50	4.6	9	6	ABR84374 Human cys
24	50	4.6	9	7	ADC17702 Cyclophil
25	50	4.6	10	3	AAY69939 Human cys

26	50	4.6	11	3	AAY69935	Aay69935 Human cys
27	50	4.6	11	3	AAY69938	Aay69938 Human cys
28	49	4.5	9	3	AAY69921	Aay69921 Human cys
29	49	4.5	9	4	AAB46930	Aab46930 Human cys
30	49	4.5	9	4	AAG68088	Aag68088 Antitumou
31	49	4.5	9	5	ABG79075	Abg79075 Human cys
32	49	4.5	9	6	ABR84373	AbR84373 Human cys
33	49	4.5	9	7	ADC17701	Adc17701 Cyclophil
34	48	4.4	8	3	AAY69950	Aay69950 Human cys
35	48	4.4	14	2	AAR72947	Aar72947 E. coli P
36	48	4.4	14	2	AAR72903	Aar72903 E. coli P
37	47	4.3	9	3	AAY69963	Aay69963 Human cys
38	47	4.3	9	4	AAB46947	Aab46947 Human cys
39	47	4.3	9	7	ADC17709	Adc17709 Modified
40	46	4.2	9	3	AAY69962	Aay69962 Human cys
41	46	4.2	9	3	AAY69941	Aay69941 Human cys
42	46	4.2	9	4	AAB46946	Aab46946 Human cys
43	46	4.2	10	3	AAY69937	Aay69937 Human cys
44	46	4.2	10	3	AAY69934	Aay69934 Human cys
45	46	4.2	11	3	AAY69933	Aay69933 Human cys

ALIGNMENTS

RESULT 1

ID	ABP74769	standard; peptide; 14 AA.
XX	ABP74769	
AC	ABP74769	
XX		
DT	03-FEB-2003	(first entry)
XX		
DE	Proteome analysis related peptide #54.	
XX		
KW	Proteome analysis; isolation; determination; diagnostic assay; detection;	
KW	protein marker; identification; metastatic; invasive cancer;	
KW	differential expression; signalling pathway; chromatography.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO200277016-A2.	
XX		
PD	03-OCT-2002.	
XX		
PF	22-MAR-2002; 2002WO-EP003368.	
XX		
PR	22-MAR-2001; 2001US-0278171P.	
PR	12-SEP-2001; 2001US-0318749P.	
PR	20-SEP-2001; 2001US-0323999P.	
XX		
PA	(VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.	
XX		
PI	Vandekerckhove J, Gevaert K;	
XX		
DR	WPI; 2003-067379/06.	
XX		
PT	Method for isolation of peptides from complex mixture of peptides	
PT	involves specific chemical and/or enzymatic alteration of at least one	
PT	type of peptide.	
XX		
PS	Example 20; Page 141; 193pp; English.	
XX		
CC	The present invention describes a method (M1) for the isolation of a	
CC	subset of peptides from a protein peptide mixture (P1). M1 involves: (a)	
CC	separating the protein peptide mixture into fractions of peptides via	
CC	chromatography; (b) chemically, or enzymatically, or chemically and	
CC	enzymatically, altering at least one amino acid of at least one of the	
CC	peptides in each fraction, thereby generating a subset of altered	
CC	peptides; and (c) isolating the altered (flagged) peptides out of each	
CC	fraction via chromatography, where the chromatography of steps (a) and	
CC	(c) is performed with the same type of chromatography. M1 can be used for	

CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular
CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 14 AA;

Query Match 7.7%; Score 83; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 HYGPGWVSMANAGK 137
Db 1 HYGPGWVSMANAGK 14

RESULT 2
AAAY69925
ID AAY69925 standard; peptide; 11 AA.

XX AC AAY69925;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #5.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.

XX PS Claim 4; Page 50; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 11 AA;

Query Match 6.6%; Score 71; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 NFKLKHYPGW 129
Db 1 NFKLKHYPGW 11
RESULT 3
AAAY69947
ID AAY69947 standard; peptide; 10 AA.
XX AC AAY69947;
XX DT 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #27.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.

XX PS Claim 4; Page 56; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;

Query Match 5.8%; Score 63; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KLKHYPGWV 130

Db 1 KLKHYPGWV 10

RESULT 4

ABR84352

ID ABR84352 standard; peptide; 10 AA.

XX AC ABR84352;

XX DT 06-NOV-2003 (first entry)

XX DE Human CypB HLA-A2 epitope, SEQ ID NO:3.

XX KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
XX KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
XX KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
XX KW human; human leukocyte antigen; HLA-A2 epitope.

XX OS Homo sapiens.

XX XX

PN JP2002365286-A.
 XX 18-DEC-2002.
 XX
 PF 18-SEP-2001; 2001JP-00283413.
 XX
 PR 13-NOV-2000; 2000JP-00345094.
 XX
 PA (ITOY/) ITO Y.
 XX
 DR WPI; 2003-508315/48.
 XX
 PT A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX
 PS Example 7; Page 8; 18pp; Japanese.
 XX
 CC The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention
 XX
 SQ Sequence 10 AA;
 Query Match 5.8%; Score 63; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 KLKHYGPGWV 130
 Db |||||
 1 KLKHYGPGWV 10
 RESULT 5
 AAY69926
 ID AAY69926 standard; peptide; 11 AA.
 XX
 AC AAY69926;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Human cyclophilin B peptide fragment #6.
 XX
 DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.
 XX
 DE Human cyclophilin B peptide fragment #6.
 XX
 DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX
 PS Claim 4; Page 50; 64pp; Japanese.
 XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX
 SQ Sequence 11 AA;
 Query Match 5.8%; Score 63; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 110 IYGERFPDENF 120
 Db |||||
 1 IYGERFPDENF 11
 RESULT 6
 AAY69924
 ID AAY69924 standard; peptide; 11 AA.
 XX
 AC AAY69924;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Human cyclophilin B peptide fragment #4.
 XX
 KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.
 XX
 DE Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX
 PS Claim 4; Page 50; 64pp; Japanese.
 XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX
 SQ Sequence 11 AA;
 Query Match 5.5%; Score 60; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 79 GYKNSKFHRVI 89
 Db |||||
 1 GYKNSKFHRVI 11

RESULT 7
AAAY69928
ID AAY69928 standard; peptide; 9 AA.
XX
AC AAY69928;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #8.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX WO9967288-A1.
PN
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR
XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 5.4%; Score 58; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 HYGPGWVSM 132
Db 1 HYGPGWVSM 9
RESULT 8
AAAY69930
ID AAY69930 standard; peptide; 10 AA.
XX
AC AAY69930;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #10.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX WO9967288-A1.
PN
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR

XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 52; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;
Query Match 5.4%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 152 AWLDGKHVVF 161
Db 1 AWLDGKHVVF 10
RESULT 9
AAAY69944
ID AAY69944 standard; peptide; 11 AA.
XX
AC AAY69944;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #24.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX WO9967288-A1.
PN
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR
XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 55; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;
Query Match 5.3%; Score 57; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GLFGKTVPKTV 65
|||||
Db 1 GLFGKTVPKTV 11

RESULT 10
AA69929
ID AAY69929 standard; peptide; 10 AA.
XX AC AAY69929;
XX DT 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #9.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX PN WO9967288-A1.
XX PD 29-DEC-1999.
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.
XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.
XX Claim 4; Page 51; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

Query Match 5.1%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FFITTVKTAW 153
|||||
Db 1 FFITTVKTAW 10

RESULT 11
AA69943
ID AAY69943 standard; peptide; 11 AA.
XX AC AAY69943;
XX DT 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #23.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX PS Claim 4; Page 51; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

PN WO9967288-A1.
XX 29-DEC-1999.
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.
XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.
XX Claim 4; Page 55; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

Query Match 5.1%; Score 55; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RVIFGLFGKTV 61
|||||
Db 1 RVIFGLFGKTV 11

RESULT 12
ABG67616
ID ABG67616 standard; peptide; 14 AA.
XX AC ABG67616;
XX DT 07-OCT-2002 (first entry)
XX DE Human ADPI tryptic digest peptide #325.
XX KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.
XX OS Homo sapiens.
XX PN WO200246767-A2.
XX PD 13-JUN-2002.
XX PF 29-NOV-2001; 2001WO-GB005289.
XX PR 08-DEC-2000; 2000US-0254431P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Parekh RB, Rohlf C;
XX WPI; 2002-508575/54.
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject, comprises detecting Alzheimer disease-associated features or Alzheimer disease-associated protein isoforms in brain tissue from the subject.
XX Claim 7; Page 72; 427pp; English.

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides
XX
SQ Sequence 14 AA;

Query Match 5.0%; Score 54; DB 5; Length 14;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 88 VIKDFMIQGGDFTR 101
:| || |||||
Db 1 IIPGFMCGGDFTR 14

RESULT 13
ADA23735
ID ADA23735 standard; peptide; 14 AA.
XX
AC ADA23735;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #344.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
DR WPI; 2003-540784/51.

Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 344; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage

CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potentially, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 14 AA;

Query Match 5.0%; Score 54; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 88 VIKDFMIQGGDFTR 101
:| || |||||
Db 1 IIPGFMCGGDFTR 14

RESULT 14
AAY69949
ID AAY69949 standard; peptide; 10 AA.
XX
AC AAY69949;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #29.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.

Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 57; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

Query Match 4.9%; Score 53; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 FITTVKTAWL 154
|||||
Db 1 FITTVKTAWL 10

RESULT 15
AAAY69945
ID AAY69945 standard; peptide; 10 AA.
XX
XX AC AAY69945;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #25.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR
XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
PI
XX WPI; 2000-116932/10.
DR
XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.
PT
XX Claim 4; Page 56; 64pp; Japanese.
PS
CC This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;
Query Match 4.8%; Score 52; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 TVPKTVDFNV 69
Db 1 TVPKTVDFNV 10
XXXXXXXXXXXX
RESULT 16
AAAY69923
ID AAY69923 standard; peptide; 9 AA.
XX
XX AC AAY69923;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #3.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX

PR 25-JUN-1998; 98JP-00178449.
XX
XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
PI
XX WPI; 2000-116932/10.
DR
XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.
PT
XX Claim 4; Page 50; 64pp; Japanese.
PS
XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 4.7%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 GFGYKNSKF 85
Db 1 GFGYKNSKF 9
XXXXXXXXXXXX
RESULT 17
AAAY69955
ID AAY69955 standard; peptide; 11 AA.
XX
XX AC AAY69955;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #35.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
PI
XX WPI; 2000-116932/10.
DR
XX Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.
PT
XX Claim 4; Page 58; 64pp; Japanese.
PS
XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;
Query Match 4.7%; Score 51; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VLEGMEVVRKV 174
Db 1 VLEGMEVVRKV 11

RESULT 18
AAY69922
ID AAY69922 standard; peptide; 9 AA.
XX
AC AAY69922;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #2.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
diagnosis of tumors.
XX
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 4.6%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 RPPDENFKL 122
Db 1 RPPDENFKL 9

RESULT 20
AAB46931
ID AAB46931 standard; peptide; 9 AA.
XX
AC AAB46931;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 15; 25pp; English.
XX

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VLEGMEVVRKV 174
Db 1 VLEGMEVVRKV 11

RESULT 19
AAY69927
ID AAY69927 standard; peptide; 9 AA.
XX
AC AAY69927;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #7.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.

Query Match 4.6%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
Db 1 DFMIQGGDF 9